Figure 1

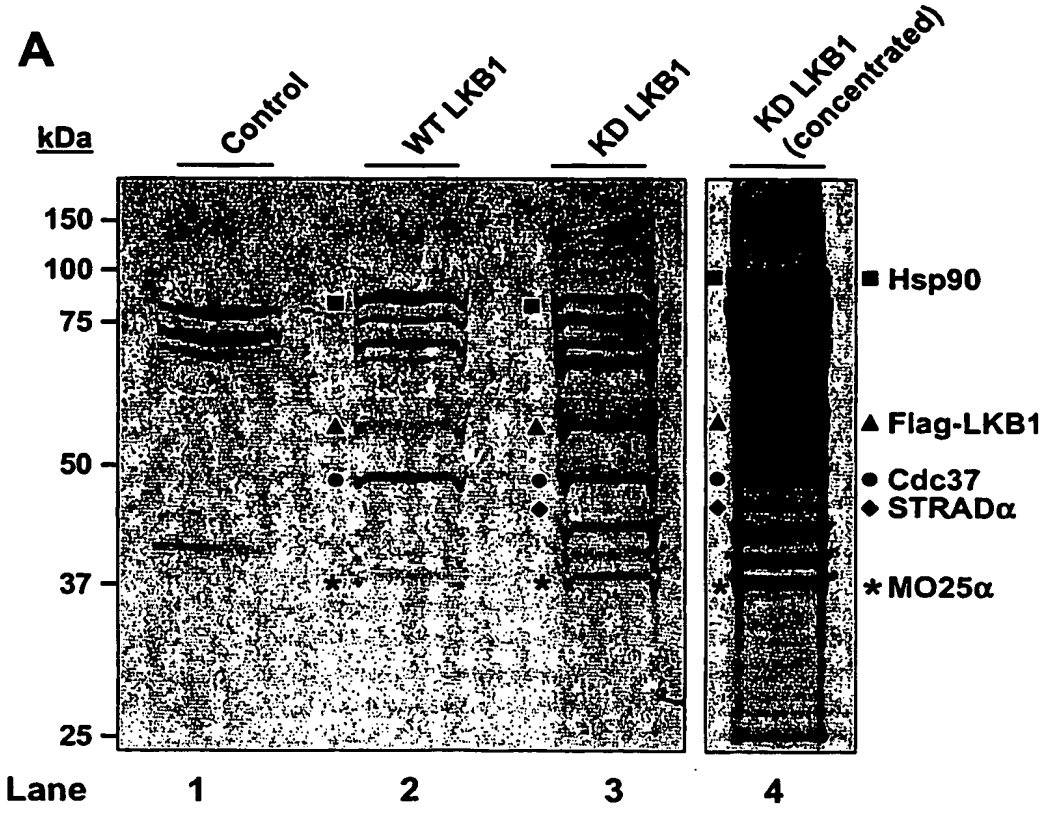


Figure 1a

B

	Protein name	Peptide matches	% sequence coverage	NCBI gi number
■	Hsp90	15/44	30%	20149594
▲	Flag-LKB1	14/46	35%	7106425
●	Cdc37	31/72	59%	5901922
◆	STRADα	11/80	34%	12060855
*	MO25α	17/37	47%	7706481

C

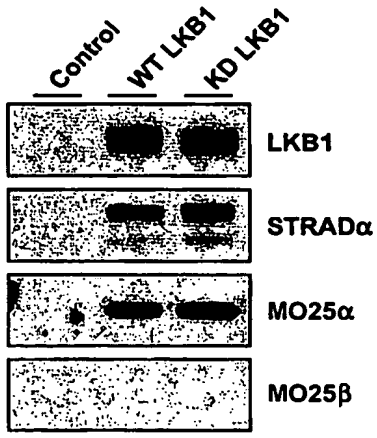


Figure 2

A

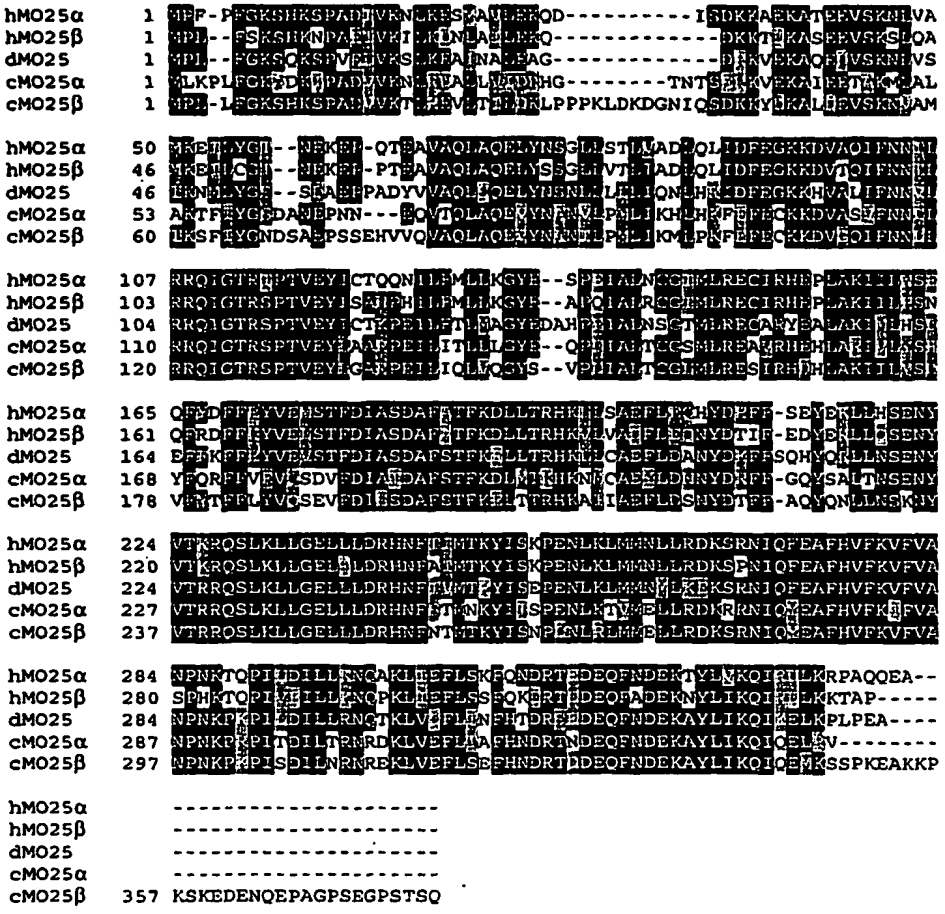


Figure 2a

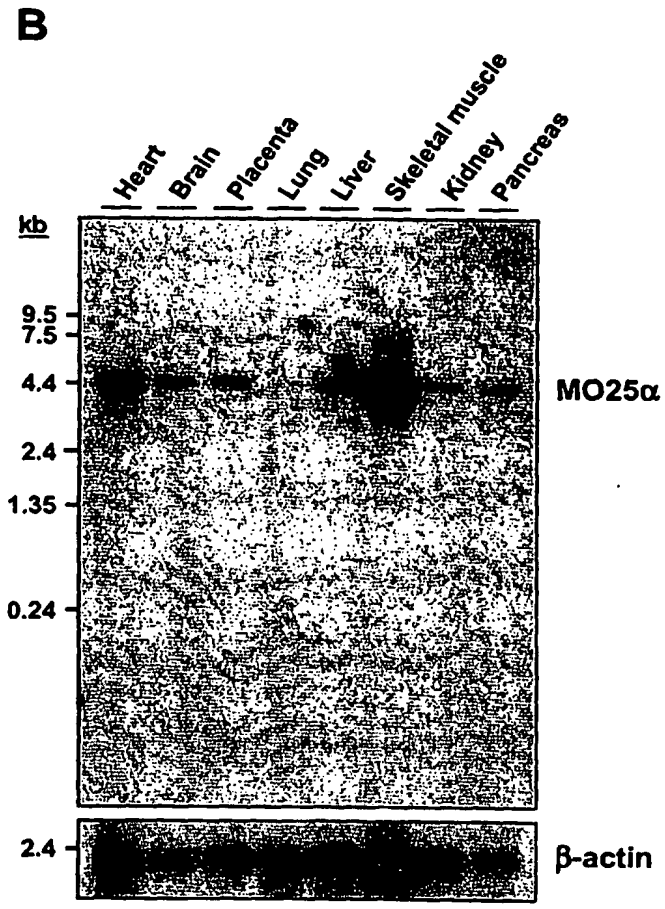
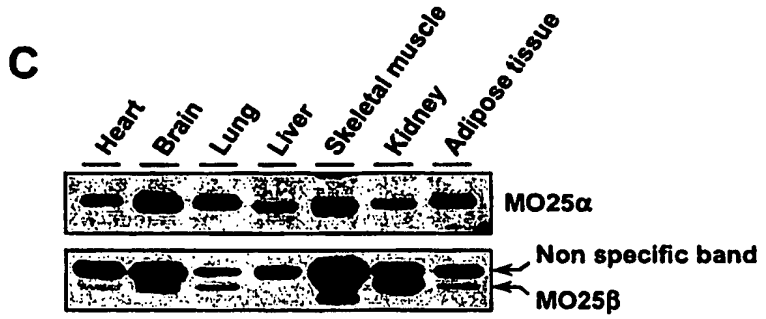

B
Heart
Brain
Placenta
Lung
Liver
Skeletal muscle
Kidney
Pancreas
kb
9.5
7.5
4.4
2.4
1.35
0.24
MO25α
2.4
β-actin

Figure 2b


C
Heart
Brain
Lung
Liver
Skeletal muscle
Kidney
Adipose tissue
MO25α
Non specific band
MO25β

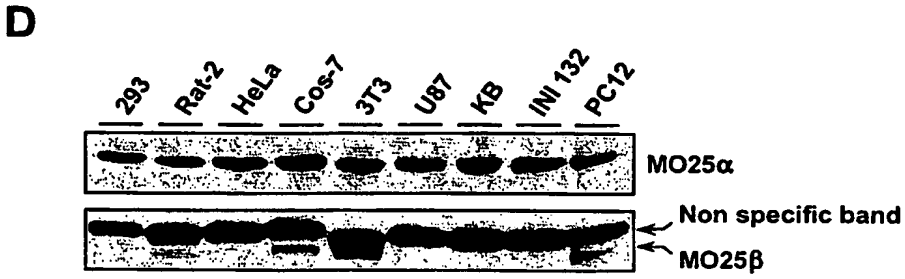

D
293
Rat-2
HeLa
Cos-7
3T3
U87
KB
INI 132
PC12
MO25α
Non specific band
MO25β

Figure 3

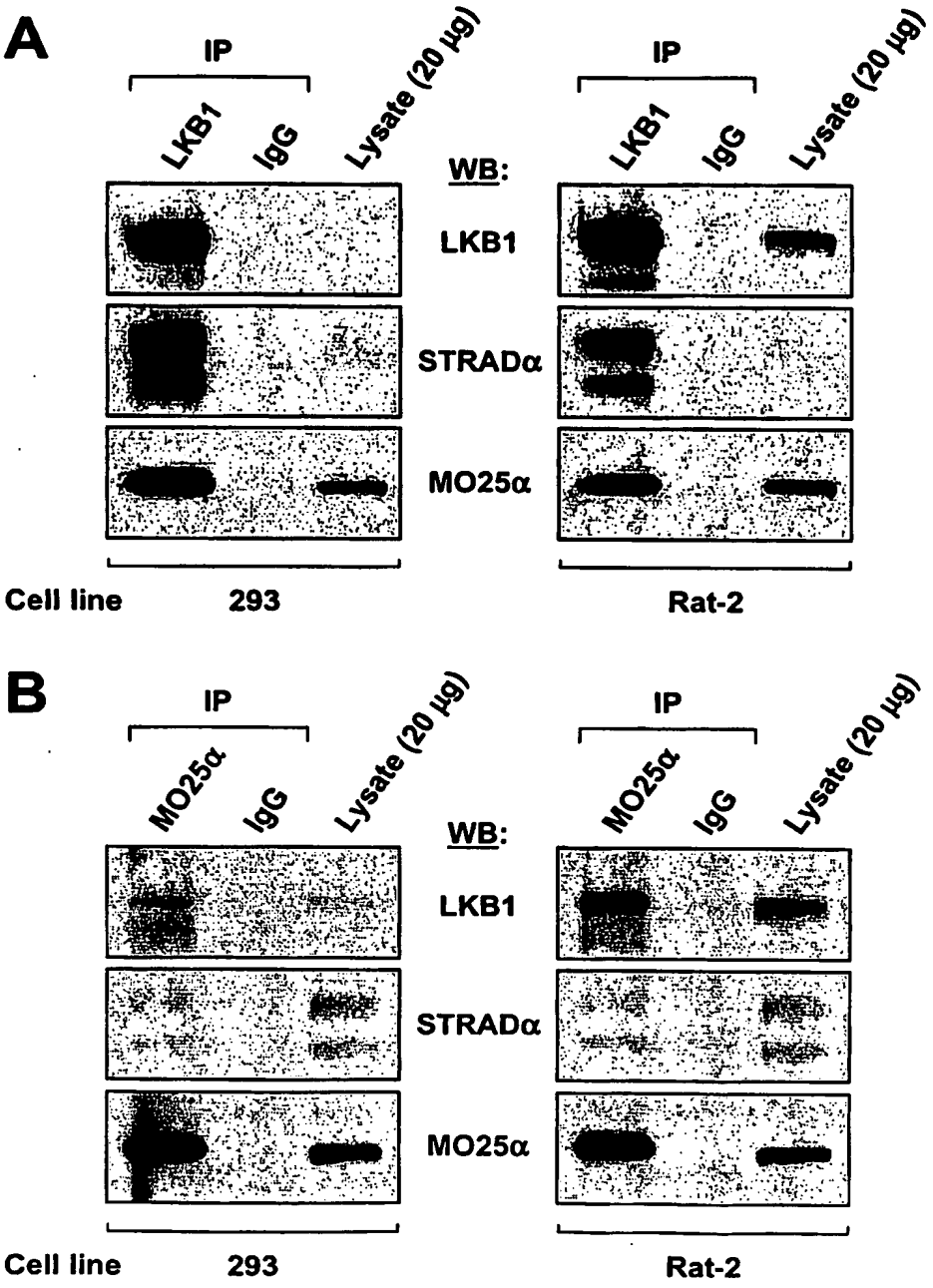
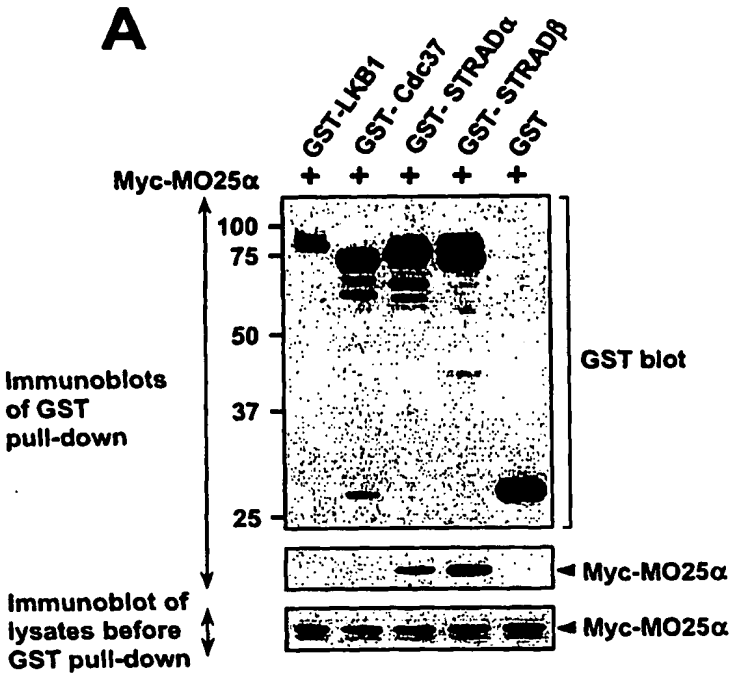

A
IP
LKB1
IgG
Lysate (20 µg)
WB:
LKB1
STRADα
MO25α
Cell line
293
Rat-2
B
IP
MO25α
IgG
Lysate (20 µg)
WB:
LKB1
STRADα
MO25α
Cell line
293
Rat-2

Figure 4


A
GST-LKB1
GST-Cdc37
GST-STRADα
GST-STRADβ
GST
Myc-MO25α
+ + + + +
100
75
50
37
25
Immunoblots of GST pull-down
GST blot
Myc-MO25α
Immunoblot of lysates before GST pull-down
Myc-MO25α

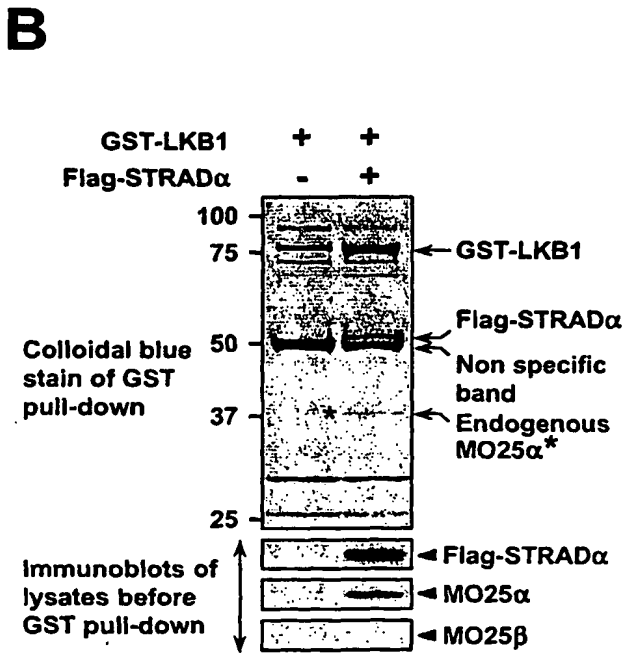

B
GST-LKB1 + +
Flag-STRADα - +
100
75
50
37
25
Colloidal blue stain of GST pull-down
GST-LKB1
Flag-STRADα
Non specific band
Endogenous MO25α*
Immunoblots of lysates before GST pull-down
Flag-STRADα
MO25α
MO25β

Figure 4a

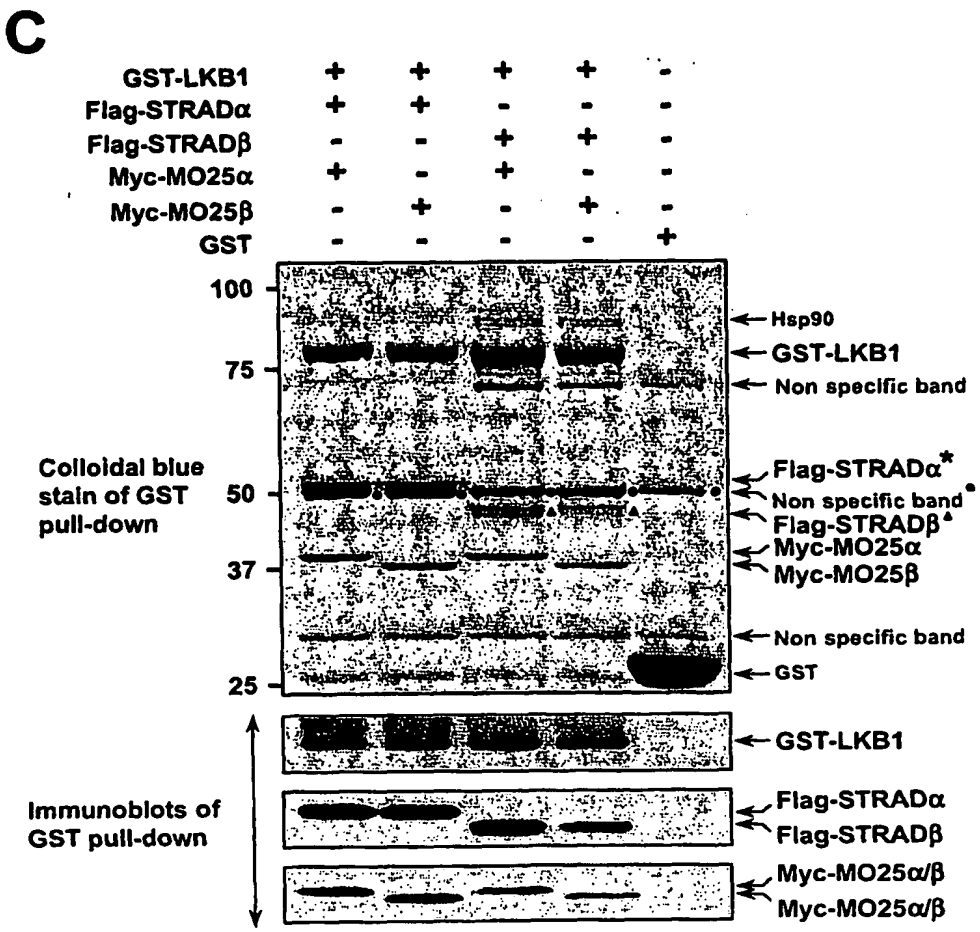

C
GST-LKB1 + + + + -
Flag-STRADα + + - - -
Flag-STRADβ - - + + -
Myc-MO25α + - + - -
Myc-MO25β - + - + -
GST - - - - +
100
75
50
37
25
Colloidal blue stain of GST pull-down
Hsp90
GST-LKB1
Non specific band
Flag-STRADα*
Non specific band
Flag-STRADβ▲
Myc-MO25α
Myc-MO25β
Non specific band
GST
Immunoblots of GST pull-down
GST-LKB1
Flag-STRADα
Flag-STRADβ
Myc-MO25α/β
Myc-MO25α/β

Figure 5

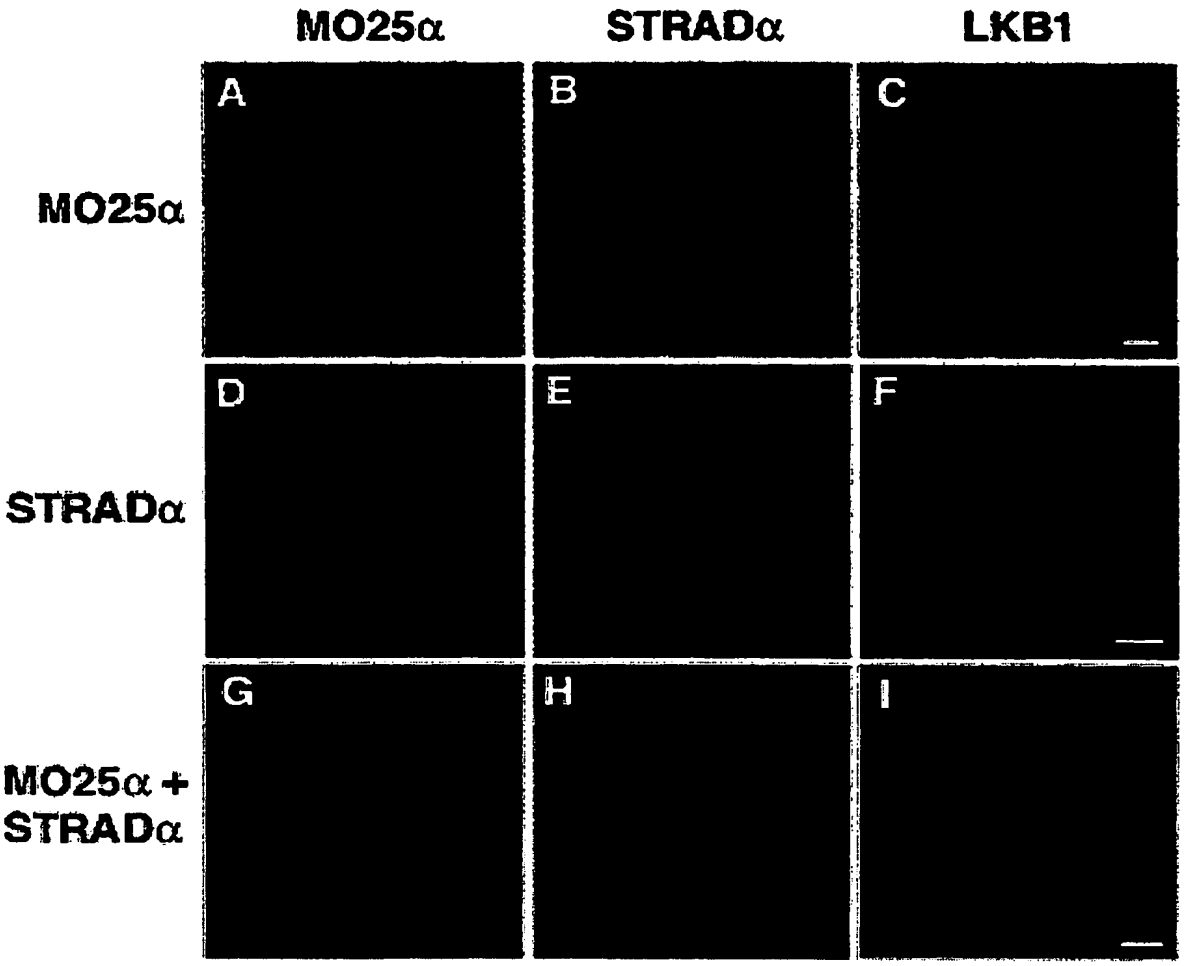


Figure 5a

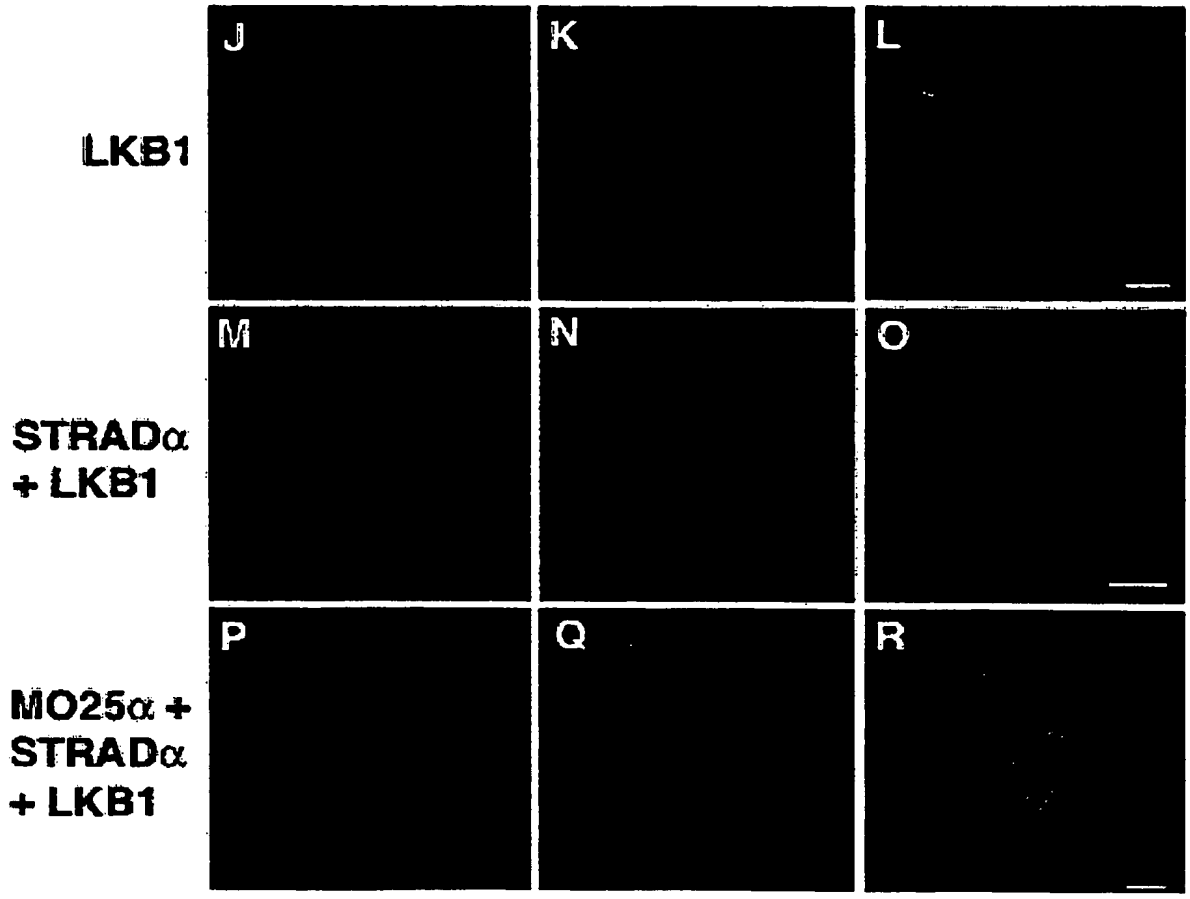
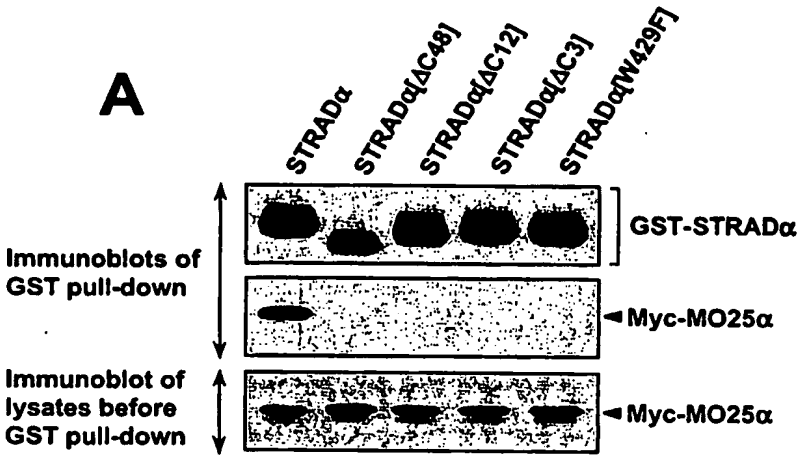


Figure 6


A
STRADα
STRADα[ΔC48]
STRADα[ΔC12]
STRADα[ΔC3]
STRADα[W429F]
GST-STRADα
Immunoblots of GST pull-down
Myc-MO25α
Immunoblot of lysates before GST pull-down
Myc-MO25α

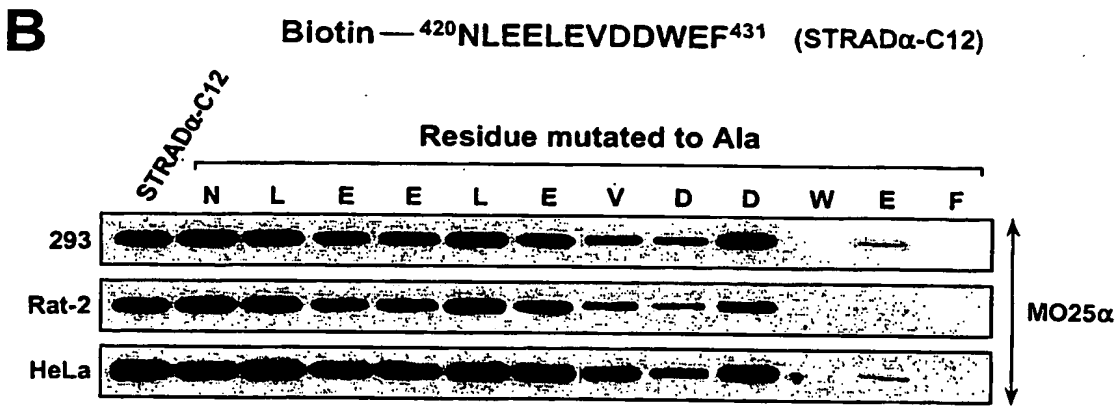

B
Biotin—420NLEELEVDDWEF431 (STRADα-C12)
STRADα-C12
Residue mutated to Ala
N L E E L E V D D W E F
293
Rat-2
HeLa
MO25α

Figure 6a

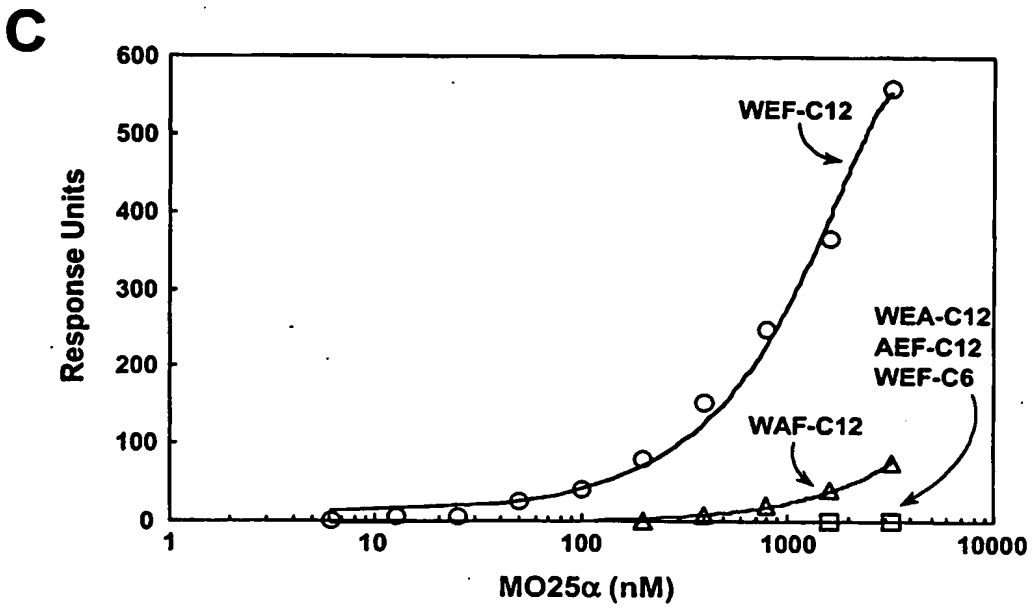

C
600
500
400
300
200
100
0
Response Units
1
10
100
1000
10000
MO25α (nM)
WEF-C12
WEA-C12
AEF-C12
WEF-C6
WAF-C12

Figure 7

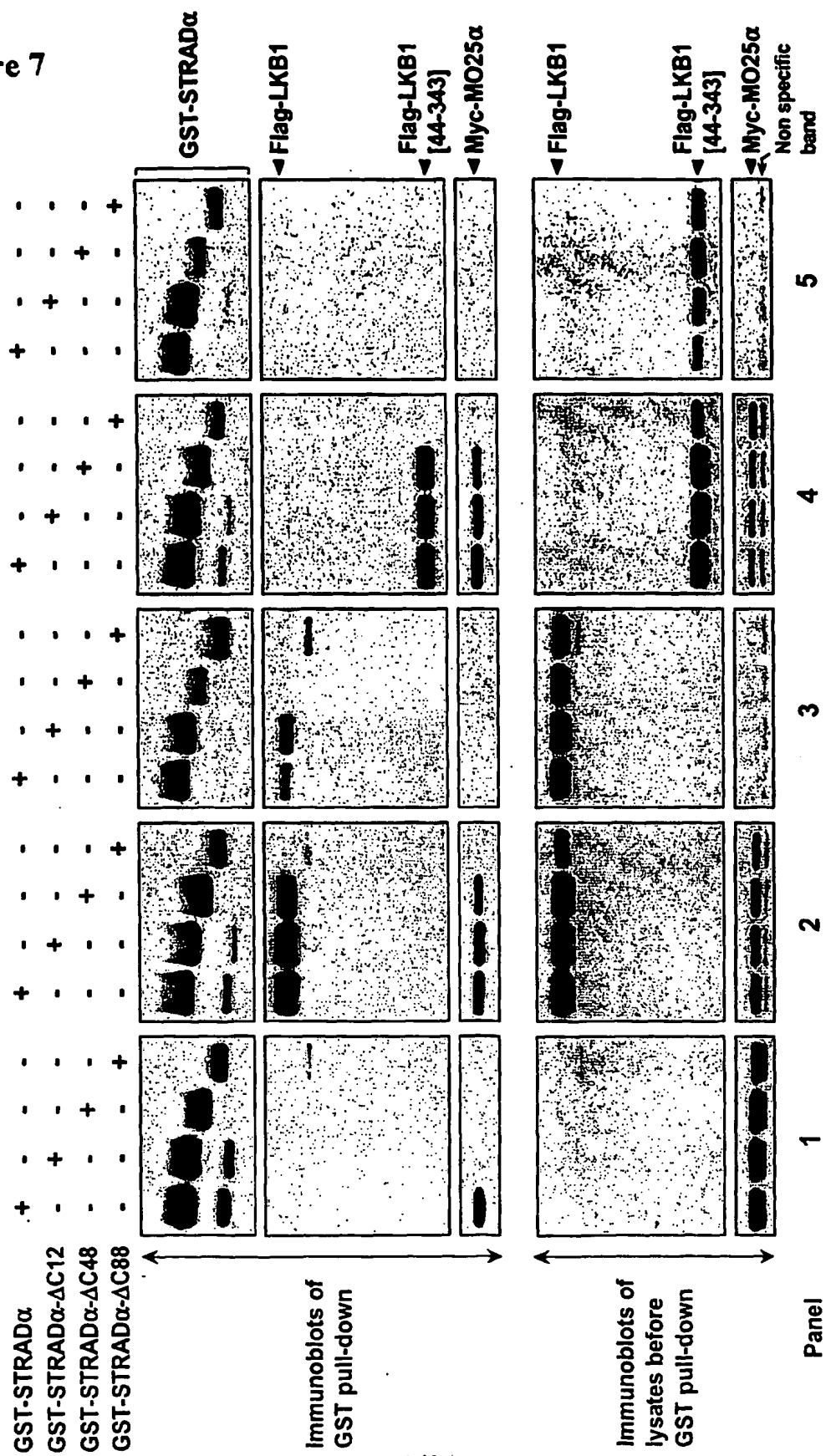

GST-STRADα
GST-STRADα-ΔC12
GST-STRADα-ΔC48
GST-STRADα-ΔC88
Myc-MO25
Myc-MO25 + Flag-LKB1
Flag-LKB1
Myc-MO25 + Flag-LKB1[44-343]
Flag-LKB1[44-343]
GST-STRADα
Flag-LKB1
Flag-LKB1 [44-343]
Myc-MO25α
Non specific band
Immunoblots of GST pull-down
Immunoblots of lysates before GST pull-down
Panel
1
2
3
4
5

Figure 8

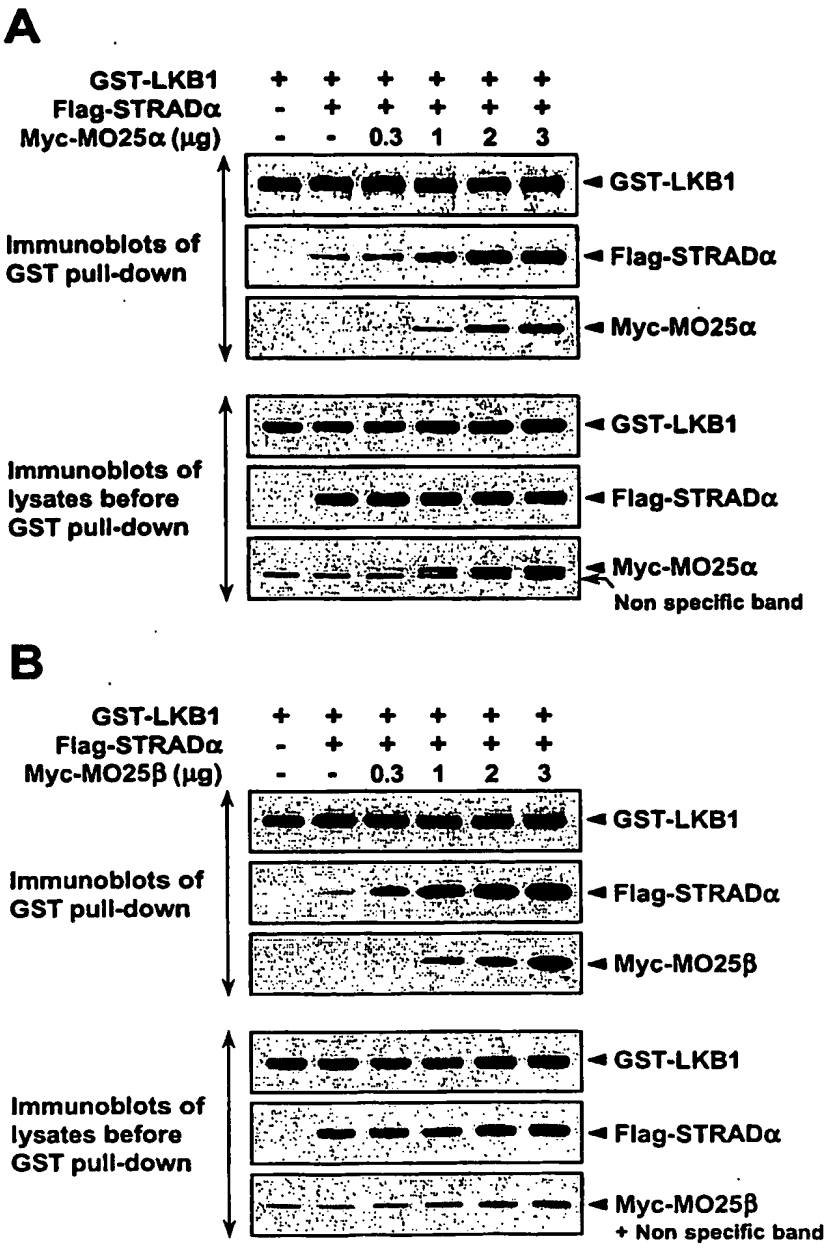

A
GST-LKB1 + + + + + +
Flag-STRADα - + + + + +
Myc-MO25α (μg) - - 0.3 1 2 3
Immunoblots of GST pull-down
GST-LKB1
Flag-STRADα
Myc-MO25α
Immunoblots of lysates before GST pull-down
GST-LKB1
Flag-STRADα
Myc-MO25α
Non specific band
B
GST-LKB1 + + + + + +
Flag-STRADα - + + + + +
Myc-MO25β (μg) - - 0.3 1 2 3
Immunoblots of GST pull-down
GST-LKB1
Flag-STRADα
Myc-MO25β
Immunoblots of lysates before GST pull-down
GST-LKB1
Flag-STRADα
Myc-MO25β
+ Non specific band

Figure 9

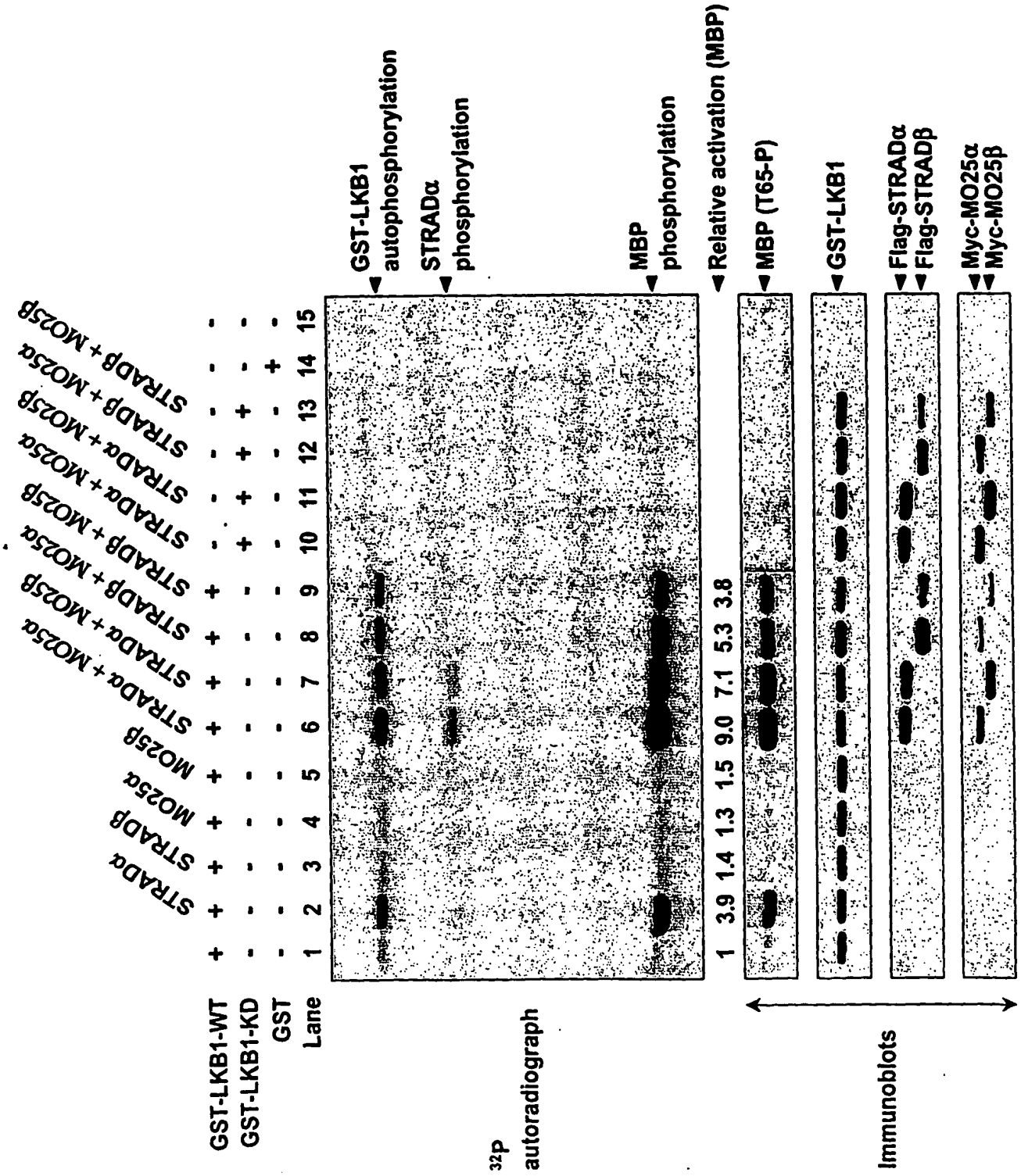

GST-LKB1 autophosphorylation
STRADα phosphorylation
MBP phosphorylation
Relative activation (MBP)
MBP (T65-P)
GST-LKB1
Flag-STRADα
Flag-STRADβ
Myc-MO25α
Myc-MO25β
Lane
GST
GST-LKB1-KD
GST-LKB1-WT
STRADα
STRADβ
MO25α
MO25β
STRADα + MO25α
STRADα + MO25β
STRADβ + MO25α
STRADβ + MO25β
1 3.9 1.4 1.3 1.5 9.0 7.1 5.3 3.8
32P autoradiograph
Immunoblots

Figure 10

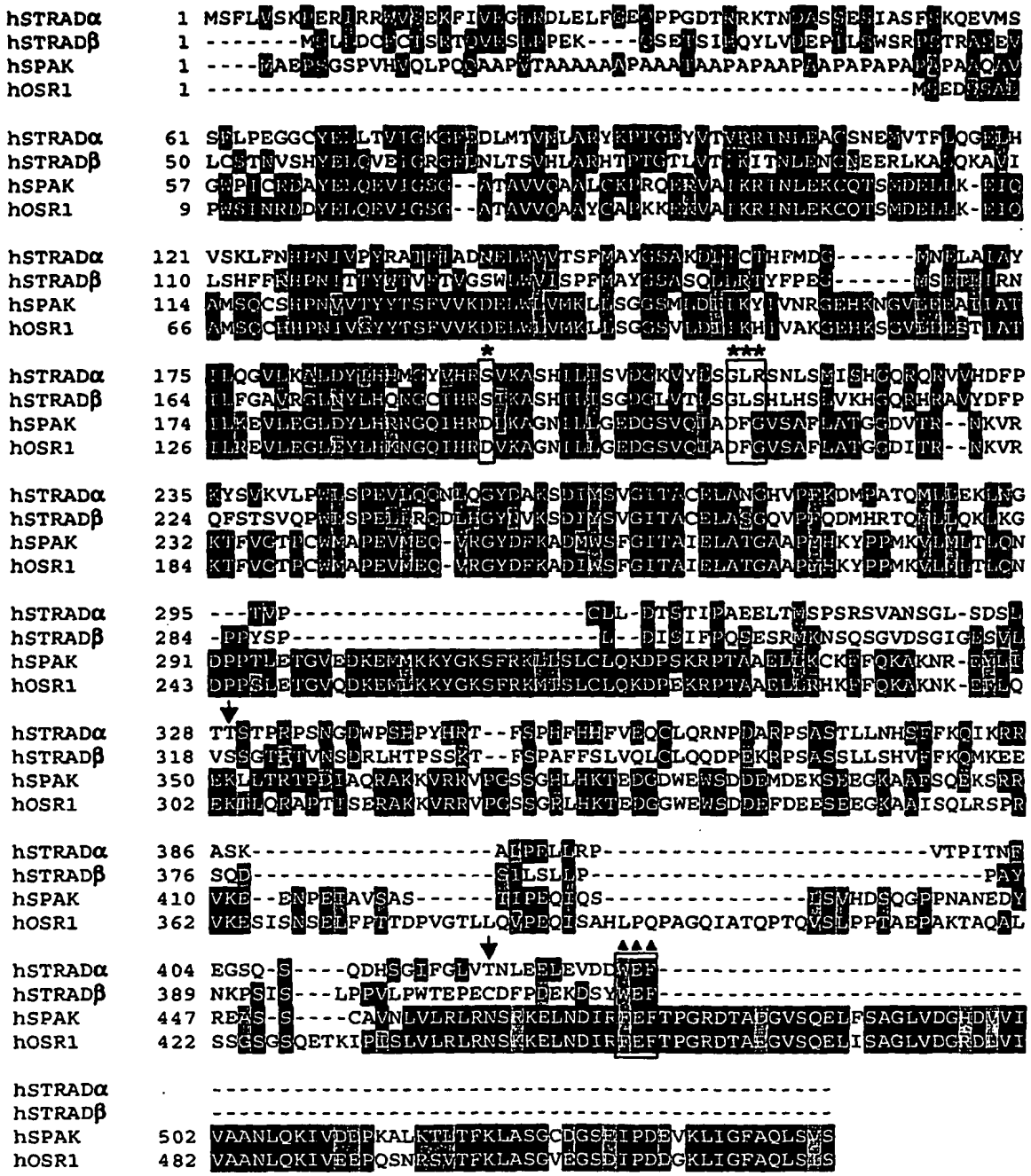


Figure 11

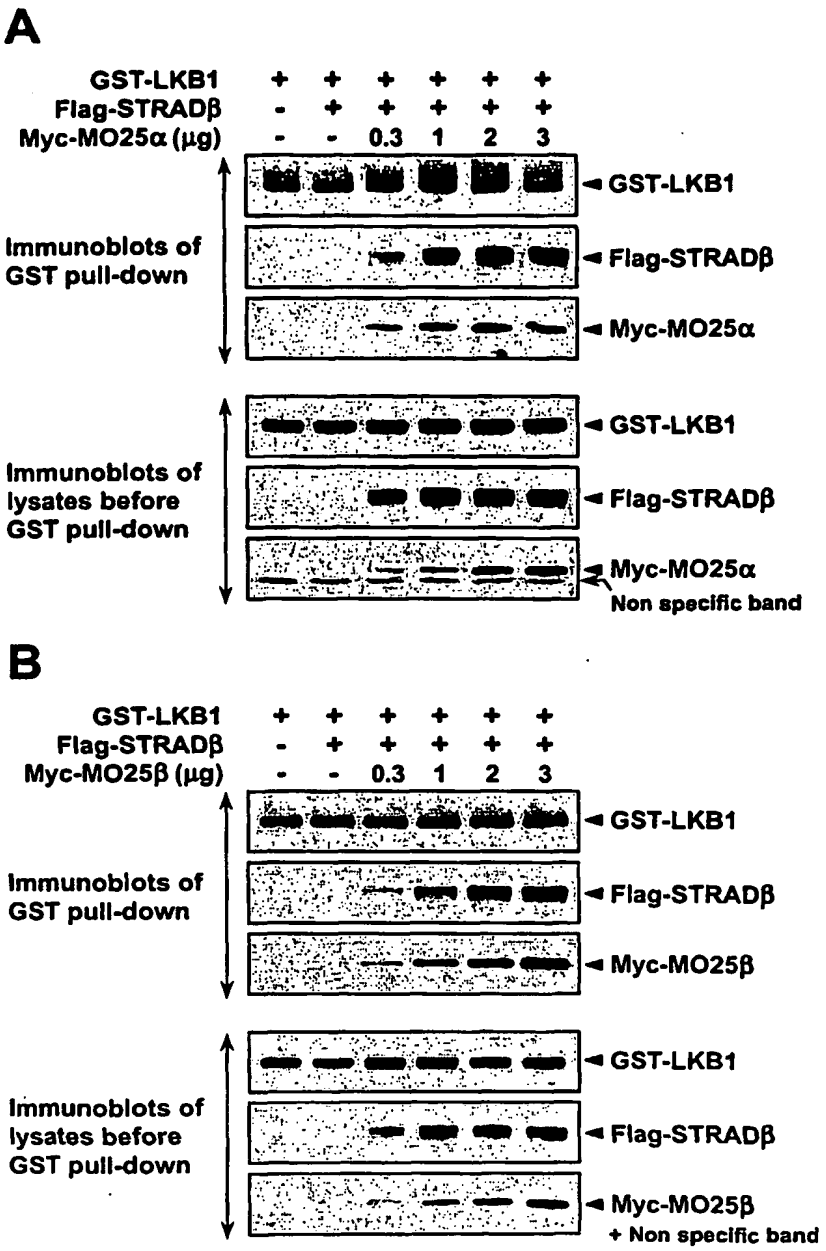

A
GST-LKB1 + + + + + +
Flag-STRADβ - + + + + +
Myc-MO25α (μg) - - 0.3 1 2 3
Immunoblots of GST pull-down
GST-LKB1
Flag-STRADβ
Myc-MO25α
Immunoblots of lysates before GST pull-down
GST-LKB1
Flag-STRADβ
Myc-MO25α
Non specific band
B
GST-LKB1 + + + + + +
Flag-STRADβ - + + + + +
Myc-MO25β (μg) - - 0.3 1 2 3
Immunoblots of GST pull-down
GST-LKB1
Flag-STRADβ
Myc-MO25β
Immunoblots of lysates before GST pull-down
GST-LKB1
Flag-STRADβ
Myc-MO25β
+ Non specific band

Figure 12

```
Tos3          11 ..LPRSSLLYNNASNSSSRIKETRKVKLLYNPLTKR.....Q...ILNNFEILATLGNGQ
Pak1          94 ..TPTTTSSFCSSGSSKNKVKETNRISLTYDPVSKR.....K...VLNTYEIIKELGHGQ
CaMKKβ       121 CICPSLPYSPVSSPQSSPRLPRRPTVESHHVSITGM.....QDCVQLNQYTLKDEIGKGS
LKB1           7 QQLGMFTEGELMSVGMDTFIHRIDSTEVIYQP..RR.....KRAKLIGKYLMGDLLGEGS
Elm1          39 TSSFGSSFSQQKPTYSTIIGENIHTILDEIRPYVKKITVSDQDKKTINQYTLGVSAGSGQ
consensus    121    p ss s   s  ss rik   tv l y pltkr     q   ilnny i   lG Gq

Tos3          61 YGKVKLARDLGTGALVAIKILNRFEKRS....GYSL.......QLKV.EN..........
Pak1         144 HGKVKLARDILSKQLVAIKIVDRHEKKQRKFFTFIK.......SSKISEN..........
CaMKKβ       176 YGVVKLAYNENDNTYYAMKVLSK..KKLIRQAGFPR.......RPPPRGTRPAPGGCIQP
LKB1          60 YGKVKEVLDSETLCRRAVKILKK..KKLRR.............................I
Elm1          99 FGYVRKAYSSTLGKVVAVKIIPKKPWNAQQYSVNQVMRQIQLWKSKGKITTNMSGNEAMR
consensus    181 yGkVkla d  t  lvAiKil k  kk  k   y           k

Tos3          99 ....PRVNQEIEVMKRCHHE.NVVELYEILNDPESTKVYLVLEYCSRGPVKWCPENKMEI
Pak1         187 ....DKIKREIAIMKKCHHK.HVVQLIEVLDDLKSRKIYLVLEYCSRGEVKWCPPDCMES
CaMKKβ       227 RGPIEQVYQEIAILKKLDHP.NVVKLVEVLDDPNEDHLYMVFELVNQGPV.......MEV
LKB1          89 PNGEANVKKEIQLLRRLRHK.NVIQLVDVLYNEEKQKMYMVMEYC......VCGMQEM.L
Elm1         159 LMNIEKCRWEIFAASRLRNNVHIVRLIECLDSPFSESIWIVTNWCSLGELQWKRDDDEDI
consensus    241     drvk EI vmkrlhh  nvv LievLddp s kvylVleycs g v wc    mei

Tos3         154 .KAVGPSILTFQQ....SRKVVLDVVSGLEYLHSQGITHRDIKPSNLLISSNGTV.KISD
Pak1         242 .DAKGPSLLSFQE....TREILRGVVLGLEYLHYQGIIHRDIKPANLLISGDGTV.KISD
CaMKKβ       279 .PTLKP..LSEDQ....ARFYFQDLIKGIEYLHYQKIIHRDIKPSNLLVGEDGHI.KIAD
LKB1         141 .DSVPEKRFPVCQ....AHGYFCQLIDGLEYLHSQGIVHKDIKPGNLLLTTGGTL.KISD
Elm1         219 LPQWKKIVISNCSVSTFAKKILEDMTKGLEYLHSQGCIHRDIKPSNILLDEEEKVAKLSD
consensus    301    v p ils  q    ar vv dvv GlEYLHsQgiiHrDIKPsNlLis dgtv KisD

Tos3         208 FG..VAM.STATGSTNIQSSHEQLLKSRALGTPAFFAPELCSTEKEY.............
Pak1         296 FG..VSLAASSTNSSDSSESLDELELAKTVGTPAFFAPEMCLGEDAFTRYNLTKENLFRG
CaMKKβ       331 FG..V.........SNEFKGS..DALLSNTVGTPAFMAPESLS..........ETRKIFSG
LKB1         195 LG..VAEALHPFAADDTCRTSQ........GSPAFQPPEIANGLDTFS.............
Elm1         279 FGSCIFTPQSLPFSDANFEDCFQRELNKIVGTPAFIAPELCHLGNSKRDFVTD.......
consensus    361 fG  v    t   s d   s     l r vGtPAF aPElc     y

Tos3         252 SC.SSAIDIWSLGVTIYCLLFGKLPFNANSGLELFDSIINKPLEFPSYEEMLNGATSGIT
Pak1         354 SCISFMIDIWAVGVTLYCLLFGMLPFFSDFELKLFEKIVNDPLKFPTFKEIQSNKVSKVS
CaMKKβ       369 K....ALDVWAMGVTLYCFVFGQCPFMDERIMCLHSKIKSQALEFPDQPDIA........
LKB1         233 ...GFKVDIWSAGVTLYNITTGLYPFEGDNIYKLFENIGKGSYAIP..............
Elm1         332 ...GFKLDIWSLGVTLYCLLYNELPFFGENEFETYHKIIEVSLSSKINGNTLNDLVIKRL
consensus    421     f iDiWslGVTlYcllfg lPF ad  l lfdkIi   l fp   em

Tos3         311 M.EEYT...DAKDLLKKLLQKDPDKRIKLADIKVHPFMC.....HYGKSDAASVL...TN
Pak1         414 CEEEYE...MAKDLLLKLLEKNPQKRMTIPAIKKHPFVS.WDFDHVPENDEKLLS...SV
CaMKKβ       417 .....E...DLKDLITRMLDKNPESRIVVPEIKLHPWVTRHGAEPLPSEDENCTLVEVTE
LKB1         276 .GDCGP...PLSDLLKGMLEYEPAKRFSIRQIRQHSWFRK...KHPPAEAPVPIPPSPDT
Elm1         389 LEKDVTLRISIQDLVKVLSRDQPIDSRNHSQISSSS.VNPVRNEGPVRRFFGRLLTKKGK
consensus    481   ee     lkDLlkkllleknP kri l  Ik hpfv     dh p  d   vl   t

Tos3         359 LETFHELKVSPP.......SSCKRVELVSLPVNSSFASLDSVYMENFDHNNLRTGADRNS
Pak1         467 LE..QKLRF...........QCNQTDQFE.PISISKHELKNAV......SGVGKKIKESV
CaMKKβ       469 EEVENSVKHIPSLATVILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKQGSEDNLQG
LKB1         329 KDRWRSMTVVPYLEDLHGADEDEDLFDIEDDIIYTQDFTVPGQVPEEEASHNGQRRGLPK
Elm1         448 KKTSGKGKDKVLVSATSKVTPSIHIDEEPDKECFSTTVLRSSPDSSDYCSSLGEEAIQVT
consensus    541  e    lk  p l          rve    pv  s   lks        s lg
```

Figure 13

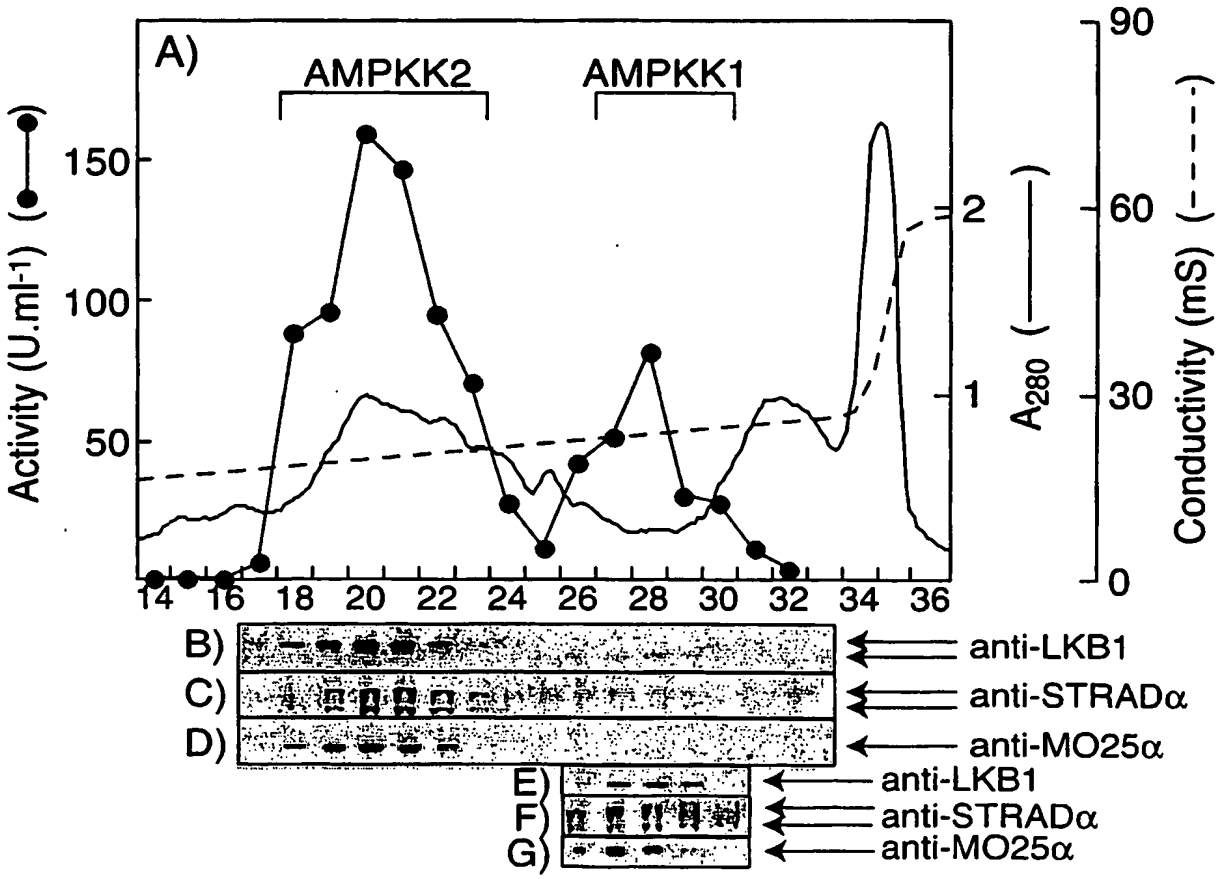

A)
AMPKK2
AMPKK1
Activity (U.ml-1)
150
100
50
2
1
A280
90
60
30
0
Conductivity (mS)
14 16 18 20 22 24 26 28 30 32 34 36
B)
C)
D)
E)
F)
G)
anti-LKB1
anti-STRADα
anti-MO25α
anti-LKB1
anti-STRADα
anti-MO25α

Figure 14

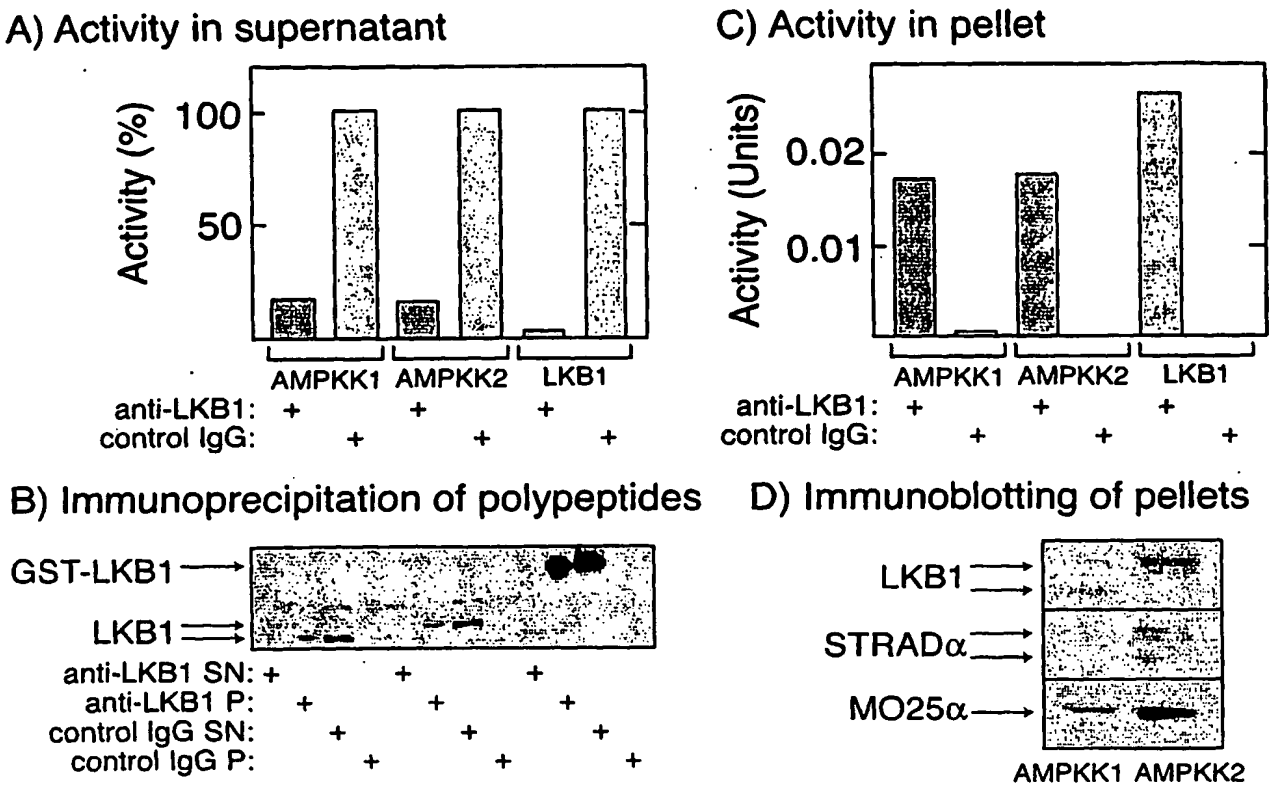

A) Activity in supernatant
Activity (%)
100
50
AMPKK1
AMPKK2
LKB1
anti-LKB1:
control IgG:
C) Activity in pellet
Activity (Units)
0.02
0.01
AMPKK1
AMPKK2
LKB1
anti-LKB1:
control IgG:
B) Immunoprecipitation of polypeptides
GST-LKB1
LKB1
anti-LKB1 SN:
anti-LKB1 P:
control IgG SN:
control IgG P:
D) Immunoblotting of pellets
LKB1
STRADα
MO25α
AMPKK1
AMPKK2

Figure 15

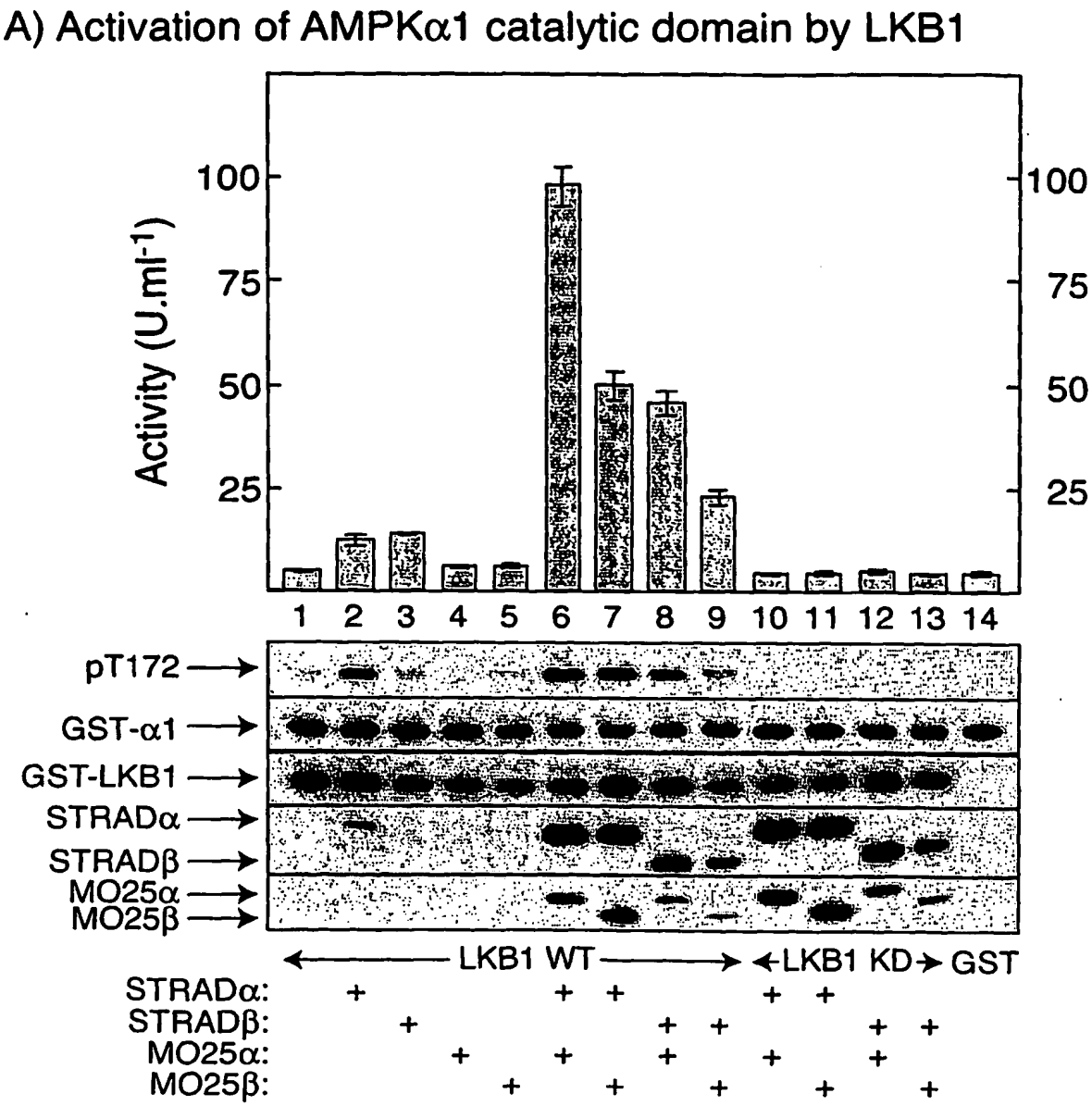

A) Activation of AMPKα1 catalytic domain by LKB1
Activity (U.ml-1)
100
75
50
25
1 2 3 4 5 6 7 8 9 10 11 12 13 14
pT172
GST-α1
GST-LKB1
STRADα
STRADβ
MO25α
MO25β
LKB1 WT
LKB1 KD
GST
STRADα:
STRADβ:
MO25α:
MO25β:

Figure 15a

B) Phosphorylation of AMPKα1 catalytic domain by LKB1

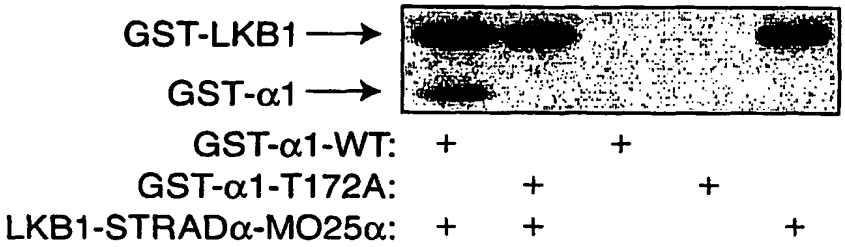


Figure 16

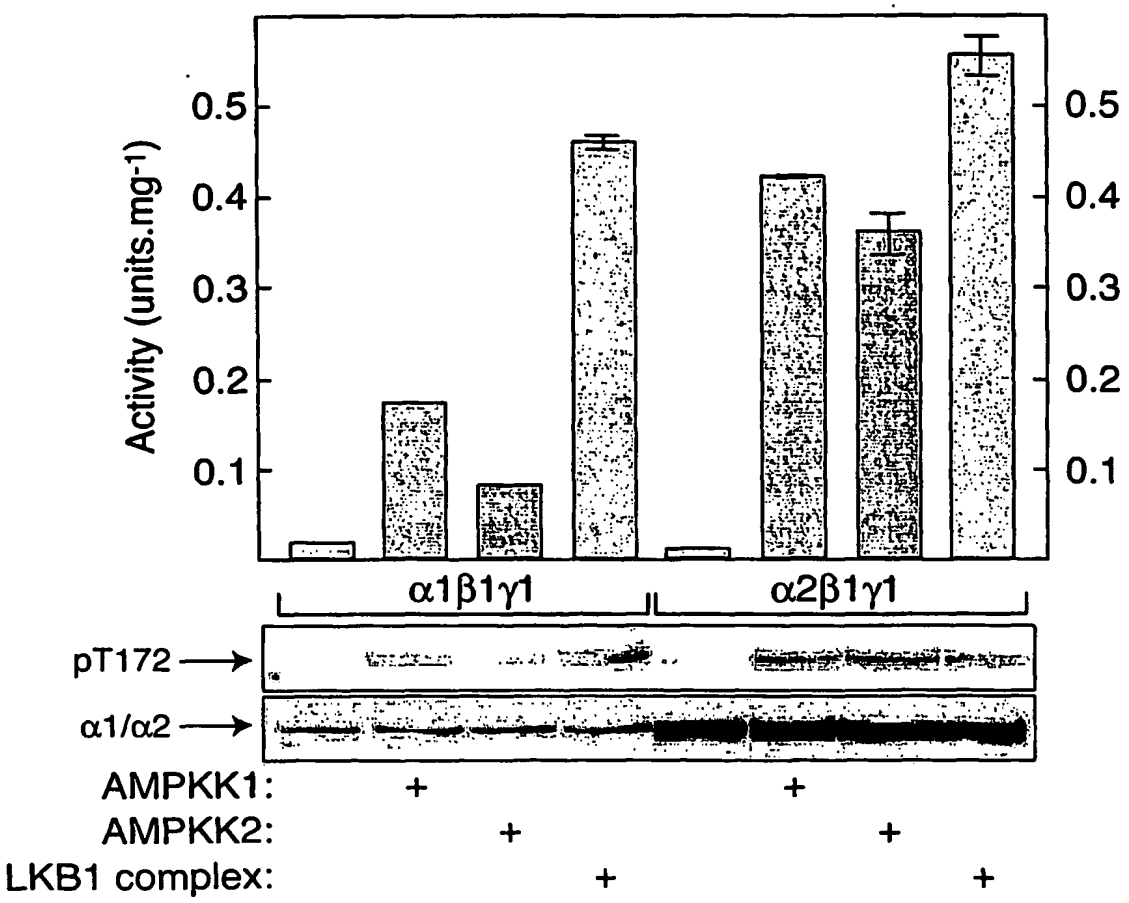

Activity (units.mg-1)
0.5
0.4
0.3
0.2
0.1
α1β1γ1
α2β1γ1
pT172
α1/α2
AMPKK1:
AMPKK2:
LKB1 complex:
+

Figure 17

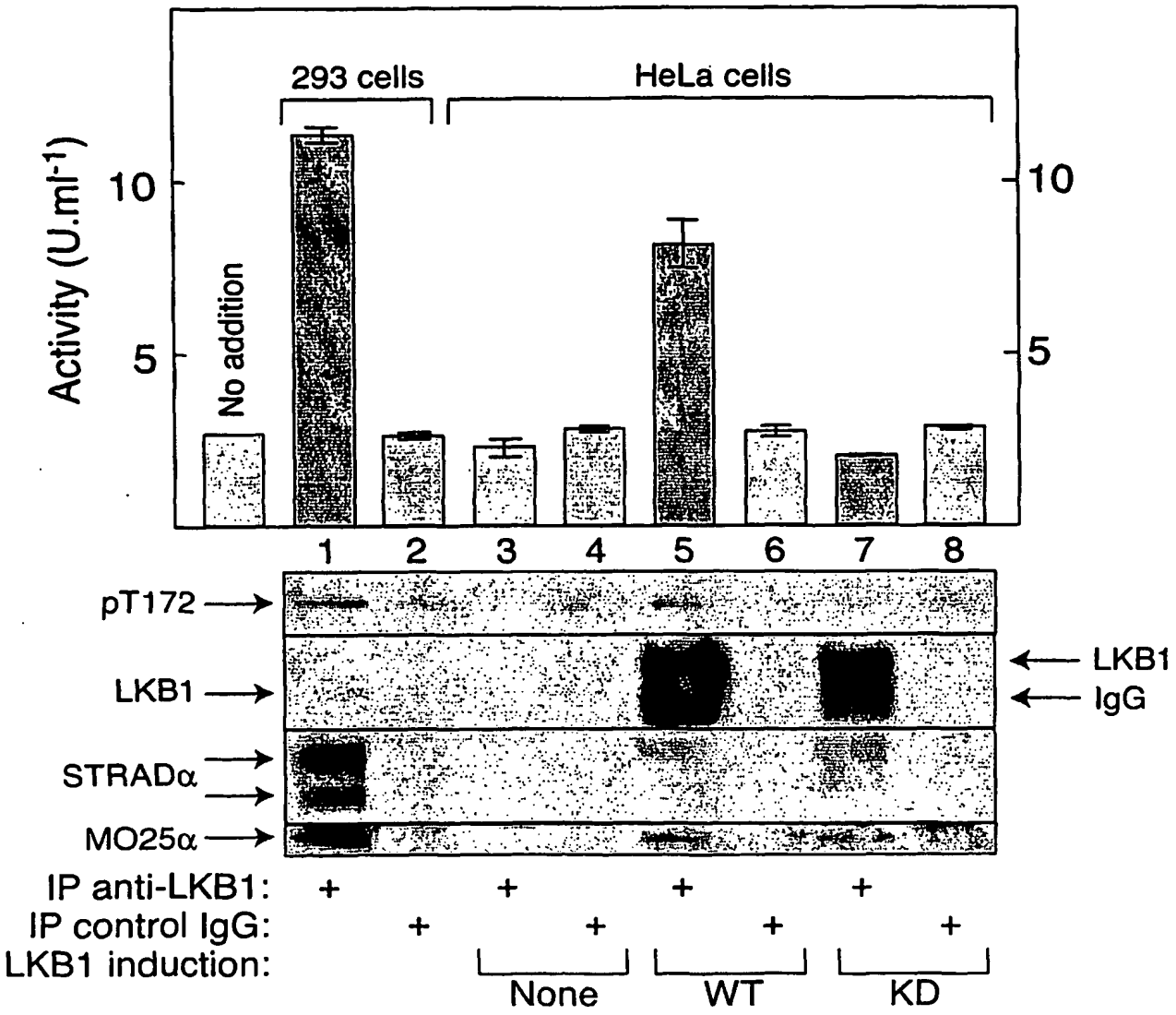

293 cells
HeLa cells
Activity (U.ml-1)
10
5
No addition
1 2 3 4 5 6 7 8
pT172
LKB1
STRADα
MO25α
LKB1
IgG
IP anti-LKB1: + + + +
IP control IgG: + + + +
LKB1 induction:
None
WT
KD

Figure 18

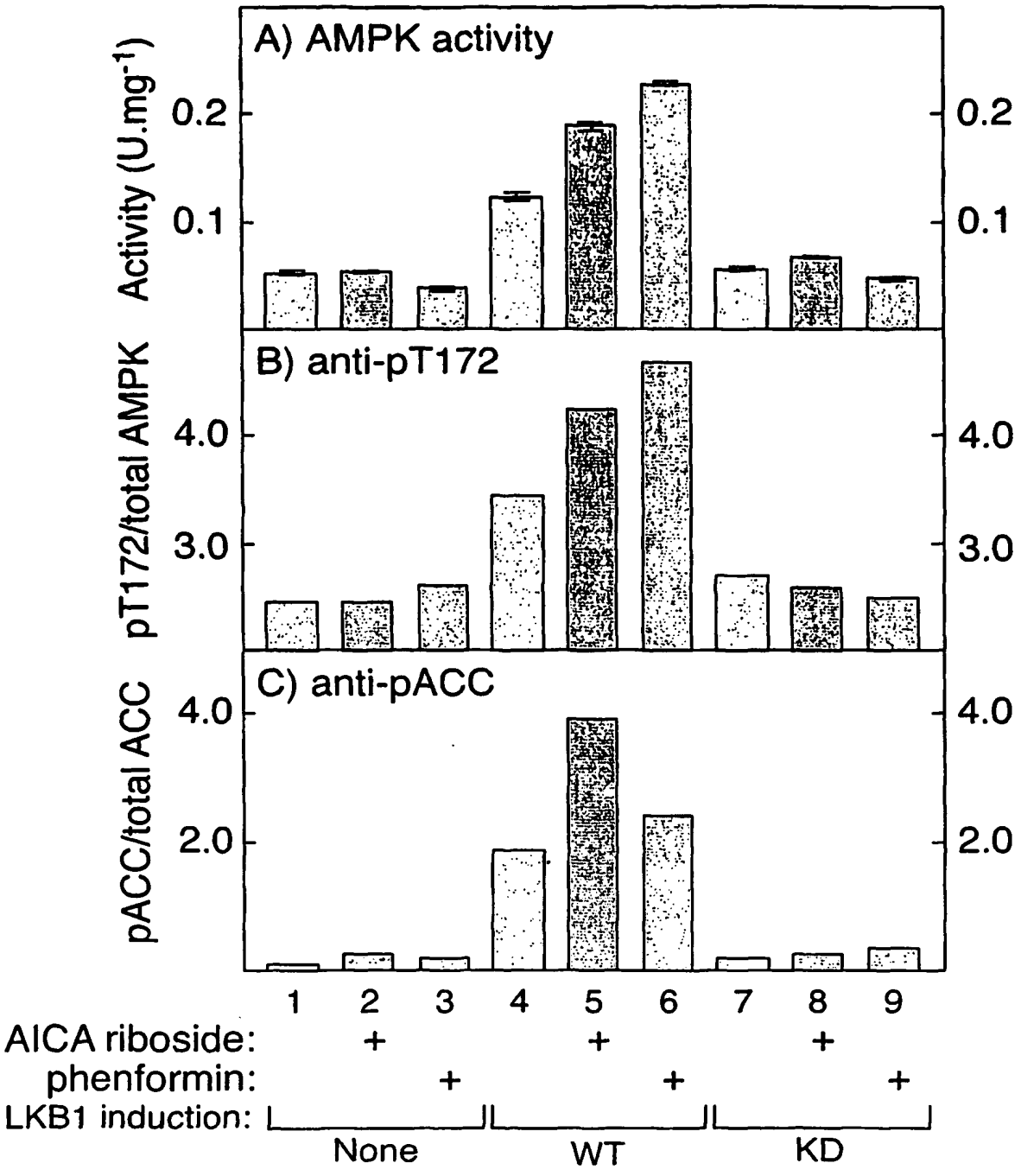

A) AMPK activity
Activity (U.mg-1)
0.2
0.1
B) anti-pT172
pT172/total AMPK
4.0
3.0
C) anti-pACC
pACC/total ACC
4.0
2.0
1 2 3 4 5 6 7 8 9
AICA riboside: + + +
phenformin: + + +
LKB1 induction:
None
WT
KD

Figure 19

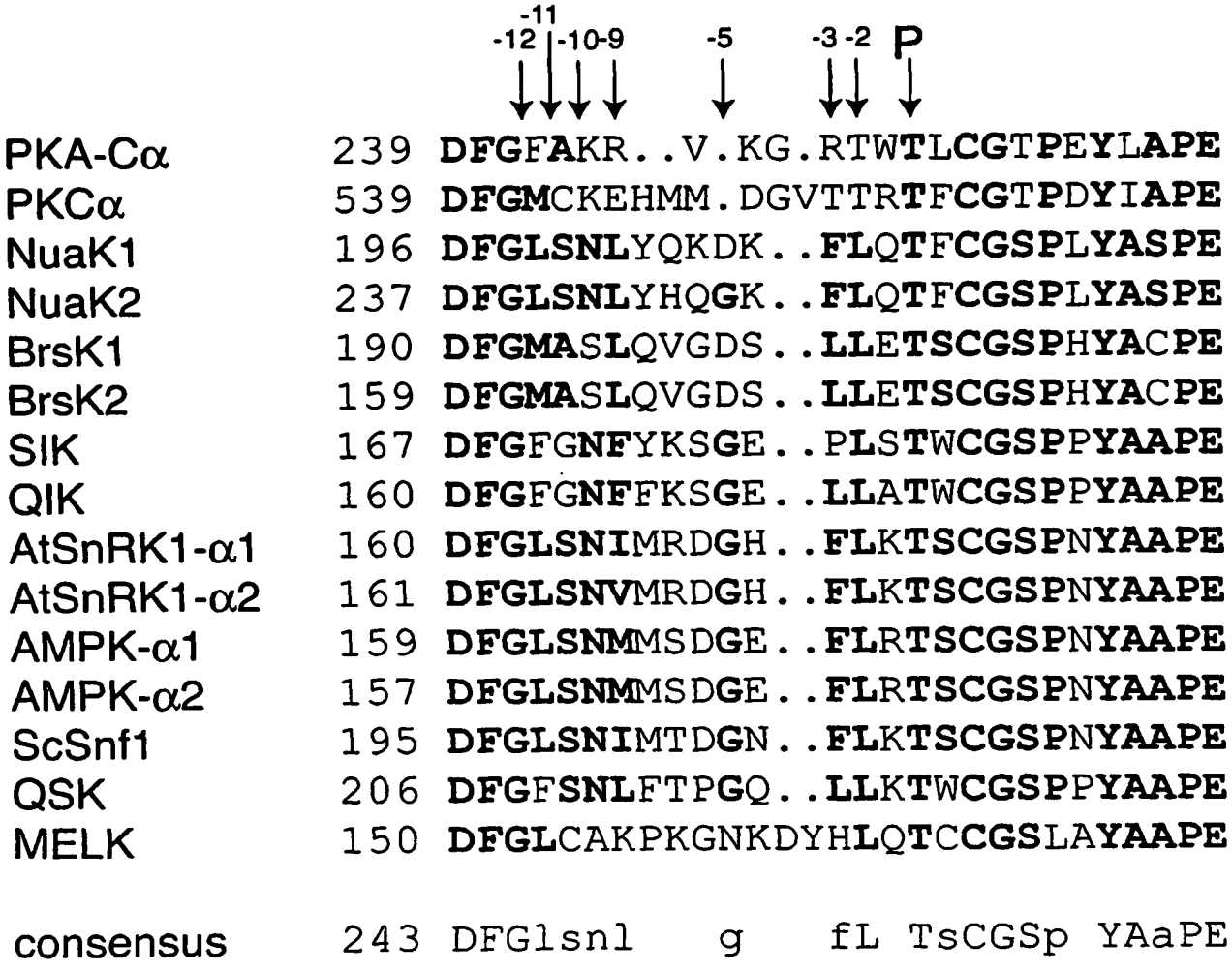
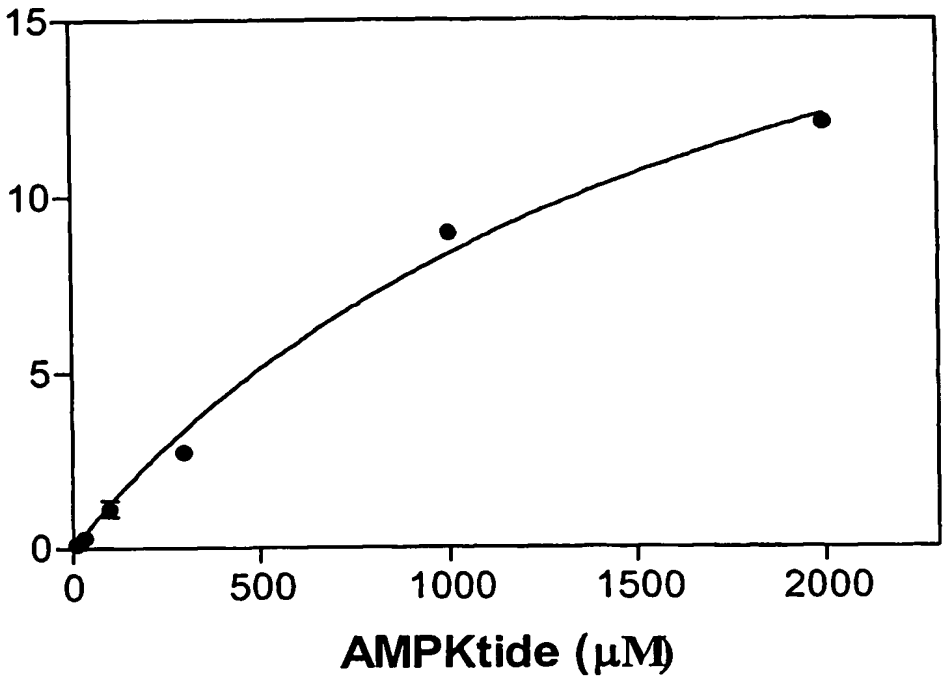

-11
-12
-10
-9
-5
-3
-2
P
PKA-Cα 239 DFGFAKR..V.KG.RTWTLCGTPEYLAPE
PKCα 539 DFGMCKEHMM.DGVTTRTFCGTPDYIAPE
NuaK1 196 DFGLSNLYQKDK..FLQTFCGSPLYASPE
NuaK2 237 DFGLSNLYHQGK..FLQTFCGSPLYASPE
BrsK1 190 DFGMASLQVGDS..LLETSCGSPHYACPE
BrsK2 159 DFGMASLQVGDS..LLETSCGSPHYACPE
SIK 167 DFGFGNFYKSGE..PLSTWCGSPPYAAPE
QIK 160 DFGFGNFFKSGE..LLATWCGSPPYAAPE
AtSnRK1-α1 160 DFGLSNIMRDGH..FLKTSCGSPNYAAPE
AtSnRK1-α2 161 DFGLSNVMRDGH..FLKTSCGSPNYAAPE
AMPK-α1 159 DFGLSNMMSDGE..FLRTSCGSPNYAAPE
AMPK-α2 157 DFGLSNMMSDGE..FLRTSCGSPNYAAPE
ScSnf1 195 DFGLSNIMTDGN..FLKTSCGSPNYAAPE
QSK 206 DFGFSNLFTPGQ..LLKTWCGSPPYAAPE
MELK 150 DFGLCAKPKGNKDYHLQTCCGSLAYAAPE
consensus 243 DFGlsnl g fL TsCGSp YAaPE

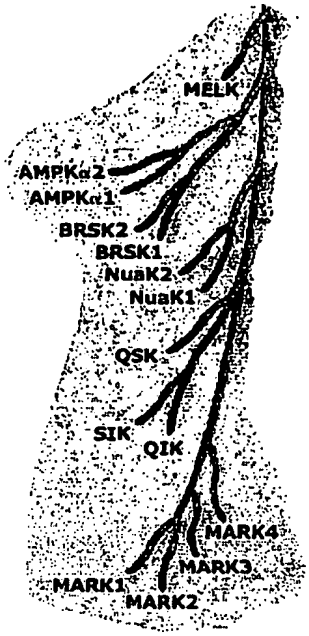
Figure 20



Km: 1.80 ± 0.48

Vmax: 23.43 ± 3.51 U/mg

Figure 21




```
                                                  *   *
AMPK1   159-DFGLSNMMSDGE--FLRTSCGSPNYAAPE
AMPK2   157-DFGLSNMMSDGE--FLRTSCGSPNYAAPE
BRSK1   174-DFGMASLQVGDS--LLETSCGSPHYACPE
BRSK2   159-DFGMASLQVGDS--LLETSCGSPHYACPE
NUAK1   196-DFGLSNLYQKDK--FLQTFCGSPLYASPE
NUAK2   193-DFGLSNLYHQGK--FLQTFCGSPLYASPE
SIK     167-DFGFGNFYKSGE--PLSTWCGSPPYAAPE
QIK     160-DFGFGNFFKSGE--LLATWCGSPPYAAPE
QSK     206-DFGFSNLFTPGQ--LLKTWCGSPPYAAPE
MARK1   200-DFGFSNEFTVGN--KLDTFCGSPPYAAPE
MARK2   160-DFGFSNEFTVGN--KLDTFCGSPPYAAPE
MARK3   196-DFGFSNEFTVGG--KLDTFCGSPPYAAPE
MARK4   198-DFGFSNEFTLGS--KLDTFCGSPPYAAPE
MELK    150-DFGLCAKPKGNKDYHLQTCCGSLAYAAPE
```

Figure 21A

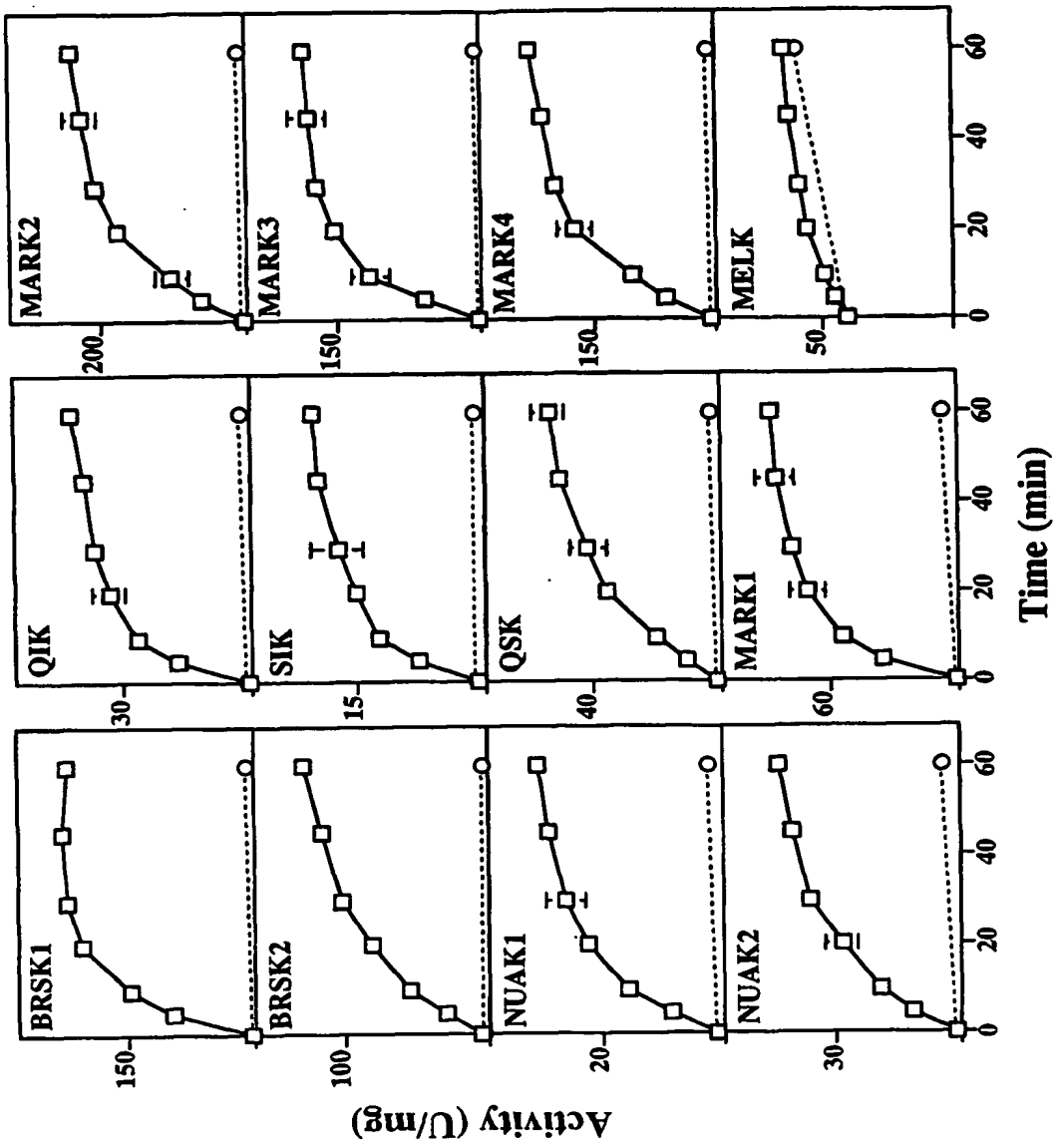

MARK2
MARK3
MARK4
MELK
QIK
SIK
QSK
MARK1
BRSK1
BRSK2
NUAK1
NUAK2
Activity (U/mg)
Time (min)

Figure 22

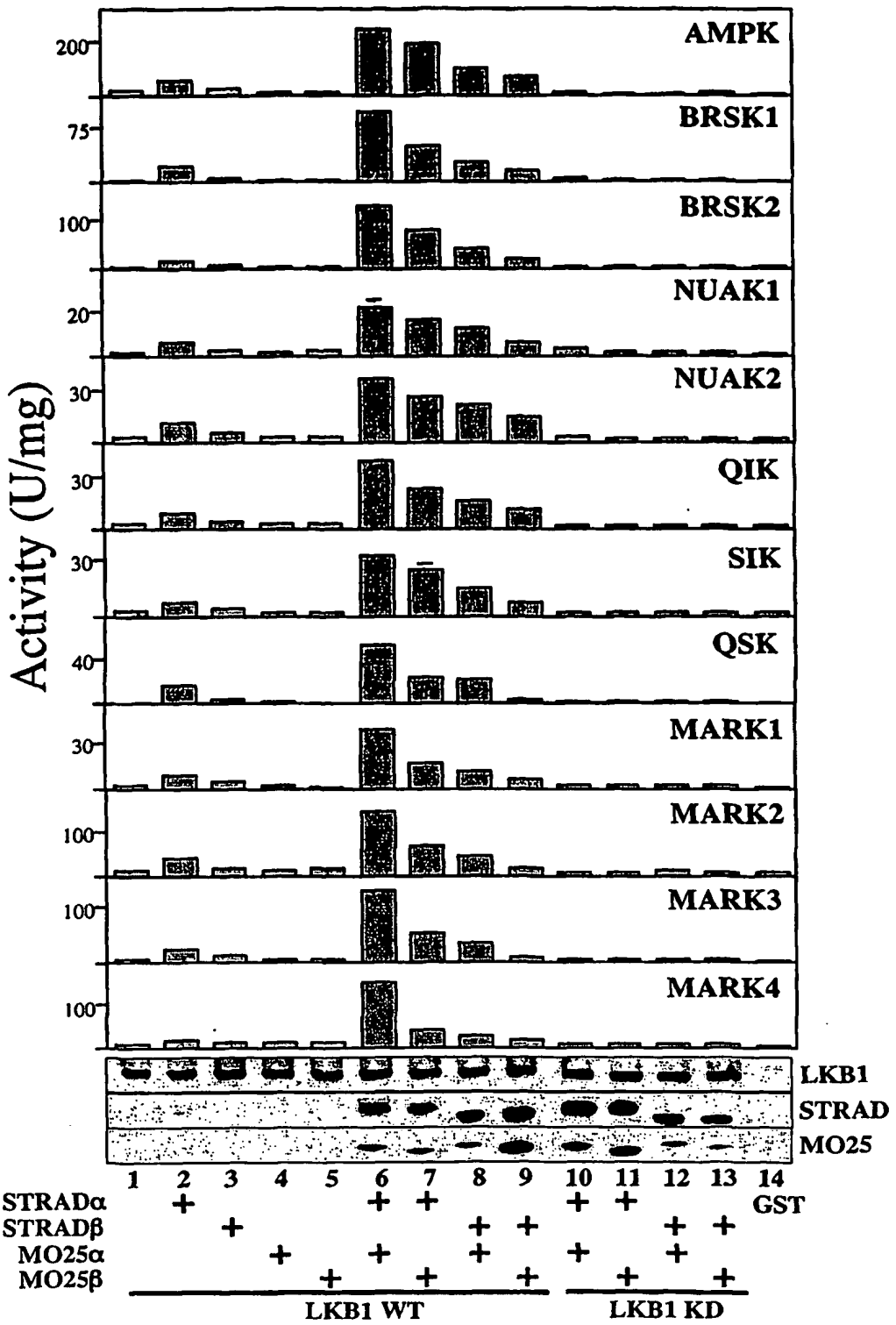

AMPK
BRSK1
BRSK2
NUAK1
NUAK2
QIK
SIK
QSK
MARK1
MARK2
MARK3
MARK4
Activity (U/mg)
200
75
100
20
30
30
30
40
30
100
100
100
LKB1
STRAD
MO25
1 2 3 4 5 6 7 8 9 10 11 12 13 14
STRADα
STRADβ
MO25α
MO25β
GST
LKB1 WT
LKB1 KD

Figure 23

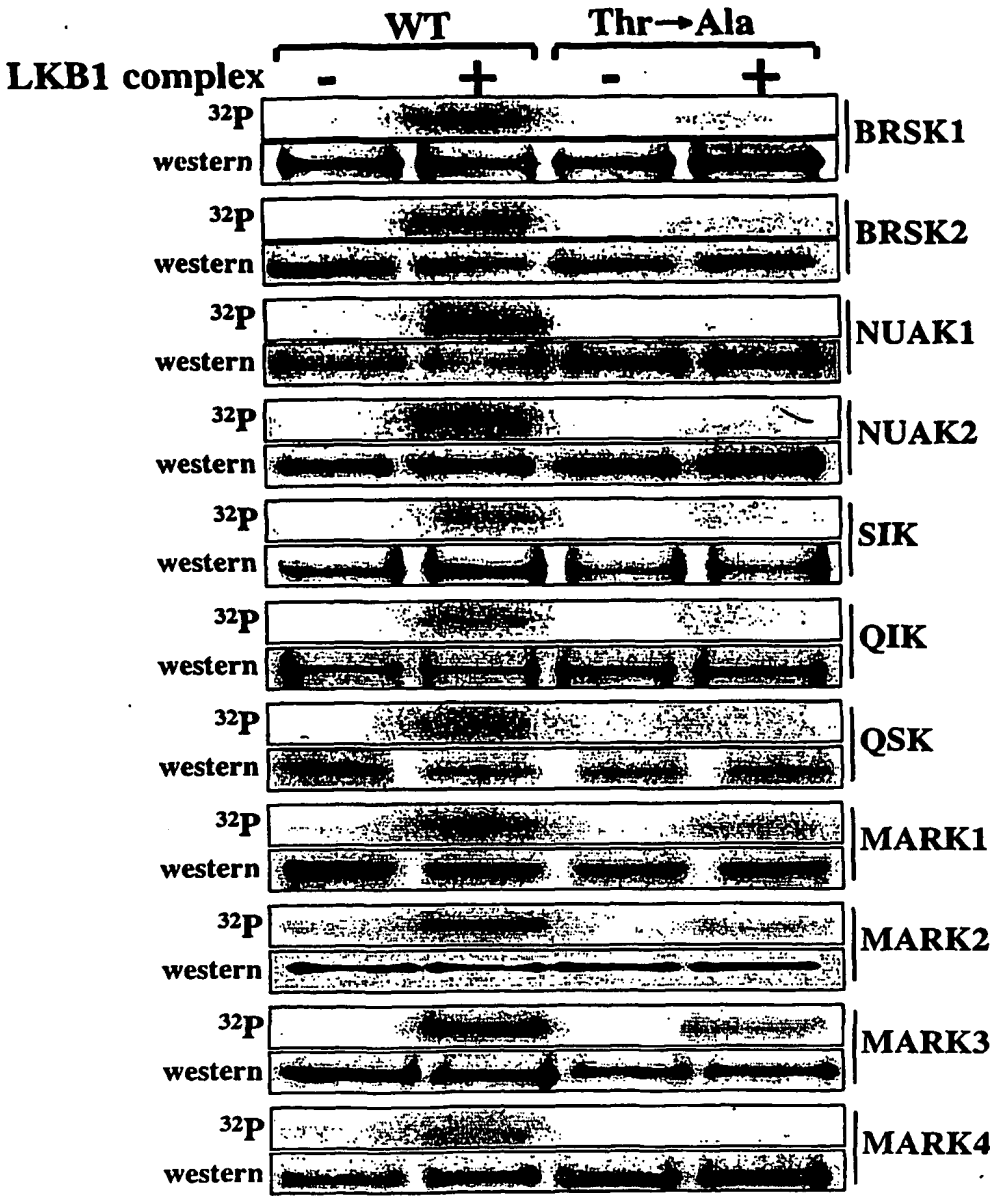

WT
Thr→Ala
LKB1 complex
-
+
-
+
32P
western
BRSK1
BRSK2
NUAK1
NUAK2
SIK
QIK
QSK
MARK1
MARK2
MARK3
MARK4

Figure 24

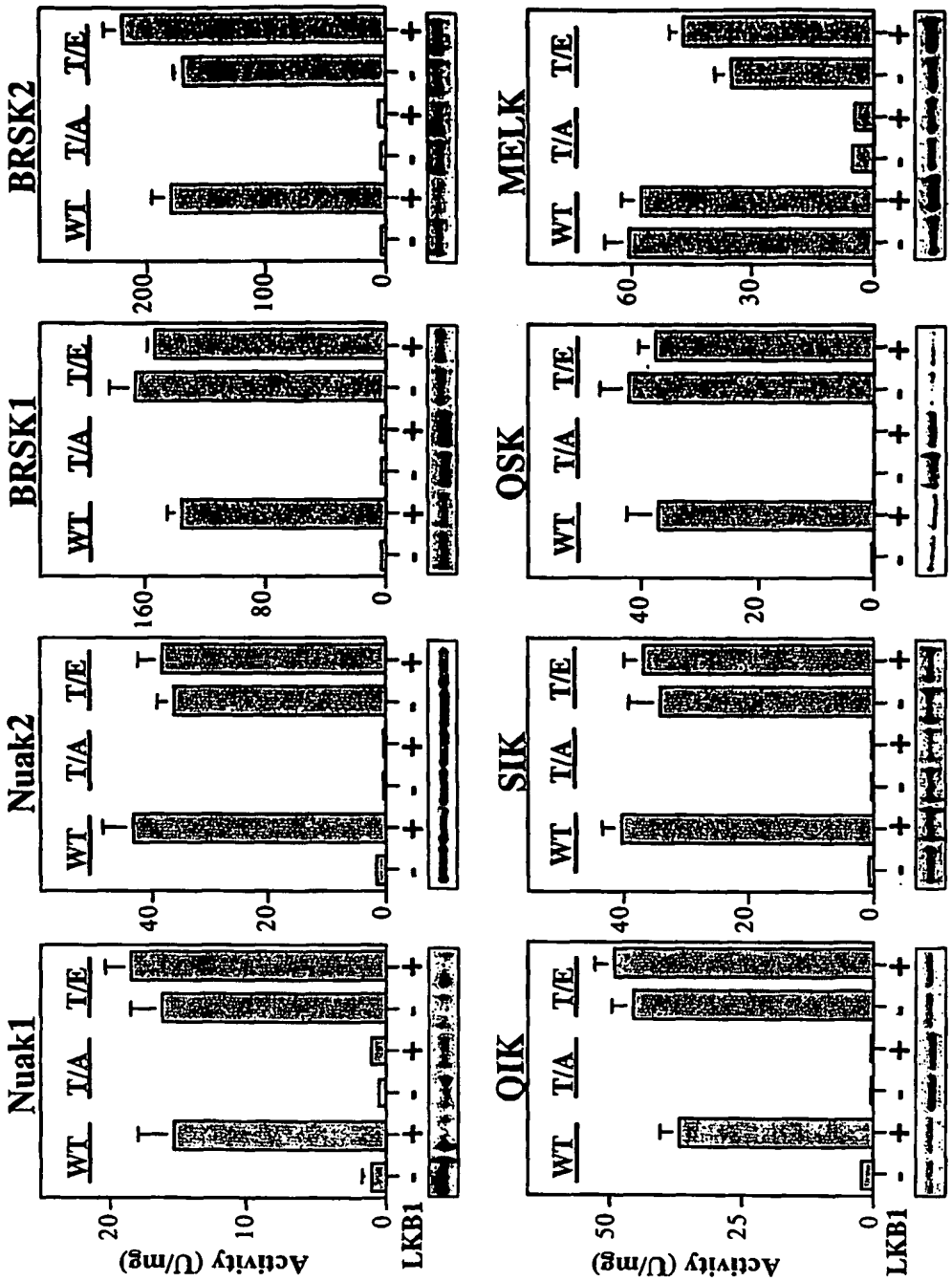

Nuak1
Nuak2
BRSK1
BRSK2
QIK
SIK
OSK
MELK
WT
T/A
T/E
Activity (U/mg)
LKB1

Figure 25

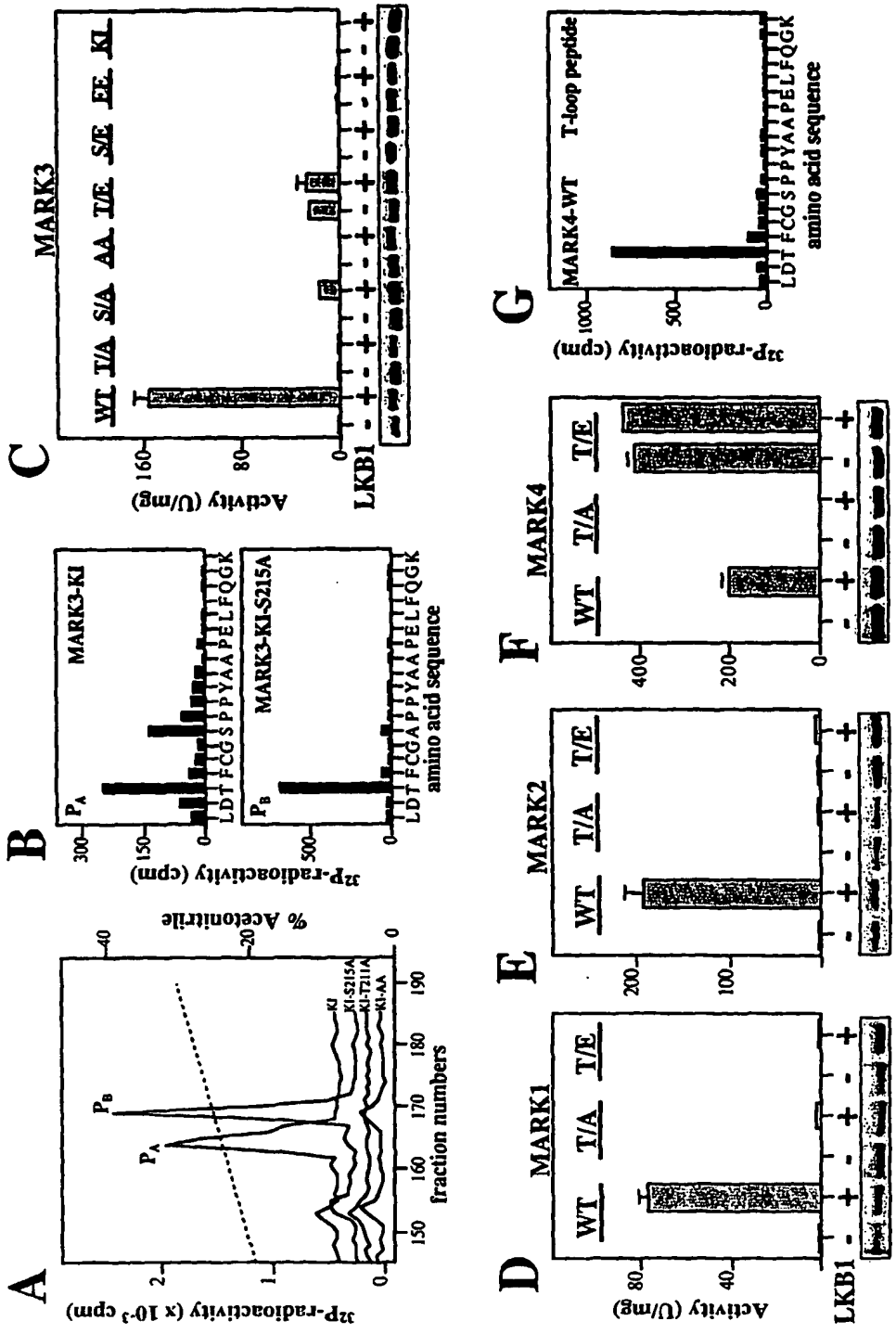

A
B
C
D
E
F
G
MARK3
MARK3-KI
MARK3-KI-S215A
MARK1
MARK2
MARK4
MARK4-WT
T-loop peptide
WT
T/A
S/A
AA
T/E
S/E
E/E
KI
LKB1
Activity (U/mg)
% Acetonitrile
fraction numbers
amino acid sequence
LDT FCG S P Y A A P E L F Q G K

Figure 26

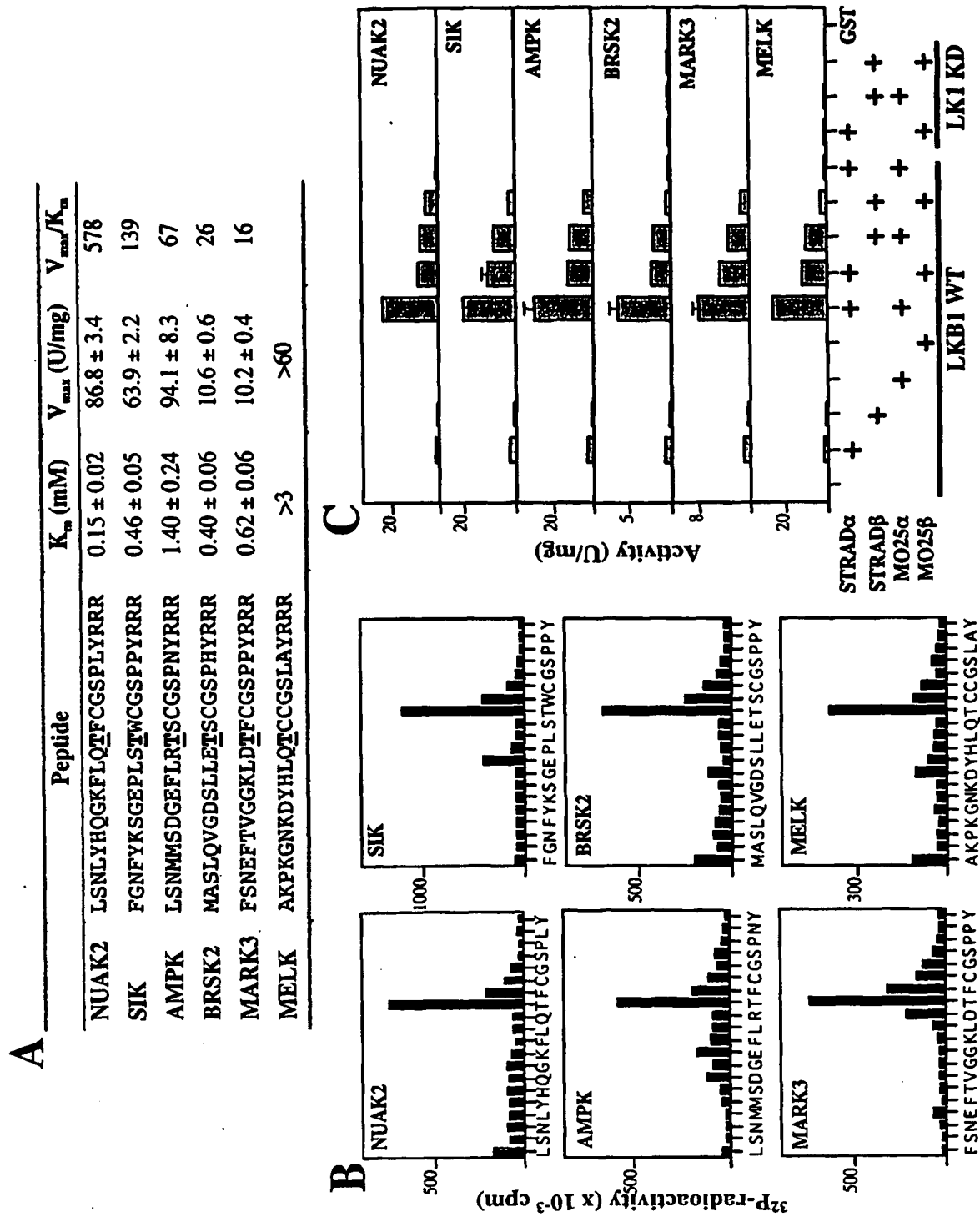

A
Peptide
K_m (mM)
V_{max} (U/mg)
V_{max}/K_m
NUAK2 LSNLYHQGKFLQTFCGSPLYRRR 0.15 ± 0.02 86.8 ± 3.4 578
SIK FGNFYKSGEPLSTWCGSPPYRRR 0.46 ± 0.05 63.9 ± 2.2 139
AMPK LSNMMSDGEFLRTSCGSPNYRRR 1.40 ± 0.24 94.1 ± 8.3 67
BRSK2 MASLQVGDSLLETSCGSPHYRRR 0.40 ± 0.06 10.6 ± 0.6 26
MARK3 FSNEFTVGGKLDTFCGSPPYRRR 0.62 ± 0.06 10.2 ± 0.4 16
MELK AKPKGNKDYHLQTCCGSLAYRRR >3 >60
B
NUAK2
SIK
AMPK
BRSK2
MARK3
MELK
32P-radioactivity (x 10-3 cpm)
amino acid sequence
C
Activity (U/mg)
NUAK2
SIK
AMPK
BRSK2
MARK3
MELK
STRADα
STRADβ
MO25α
MO25β
LKB1 WT
LK1 KD
GST

Figure 27

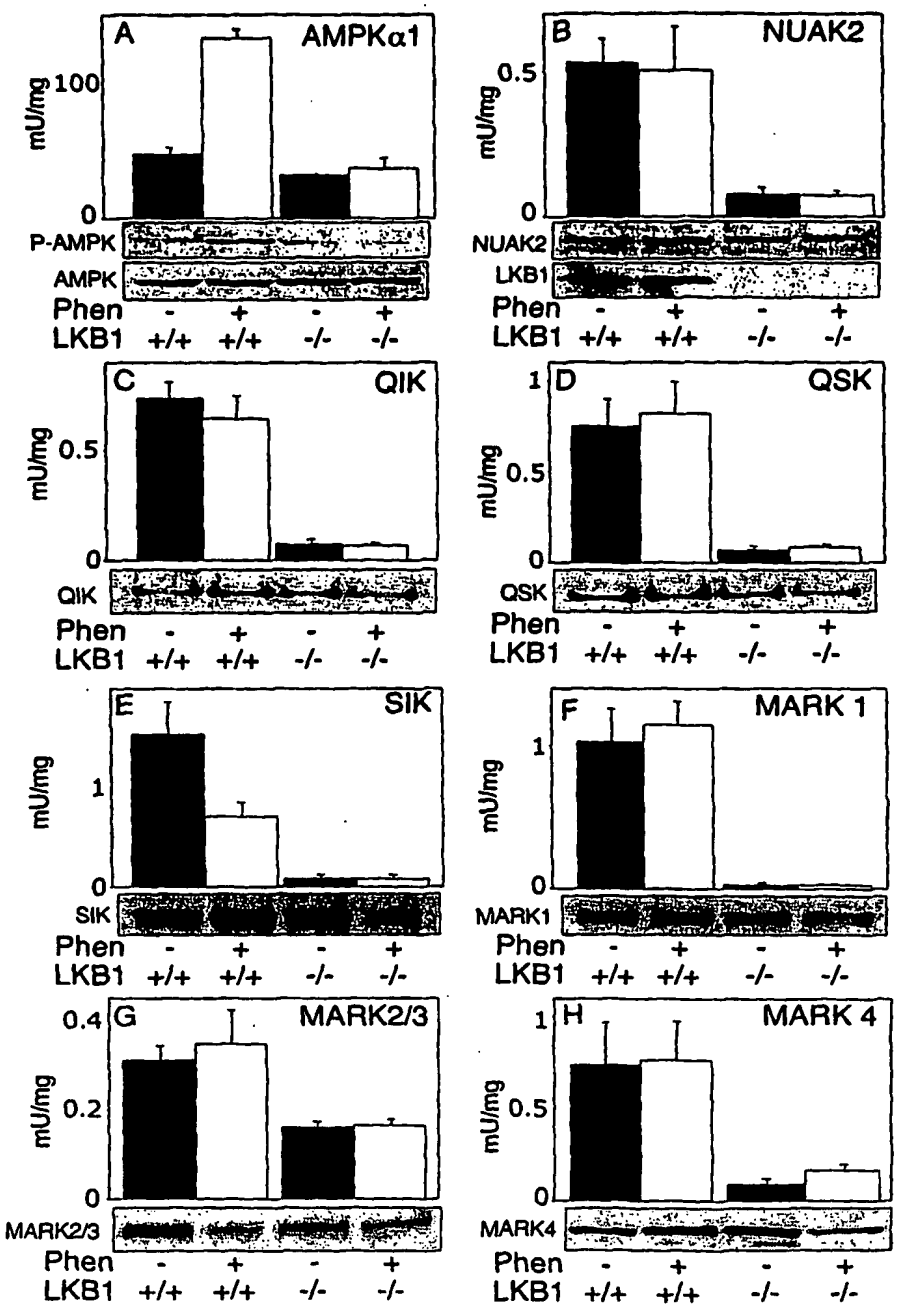

A
AMPKα1
mU/mg
100
0
P-AMPK
AMPK
Phen - + - +
LKB1 +/+ +/+ -/- -/-
B
NUAK2
mU/mg
0.5
0
NUAK2
LKB1
Phen - + - +
LKB1 +/+ +/+ -/- -/-
C
QIK
mU/mg
0.5
0
QIK
Phen - + - +
LKB1 +/+ +/+ -/- -/-
D
QSK
mU/mg
1
0.5
0
QSK
Phen - + - +
LKB1 +/+ +/+ -/- -/-
E
SIK
mU/mg
1
0
SIK
Phen - + - +
LKB1 +/+ +/+ -/- -/-
F
MARK 1
mU/mg
1
0
MARK1
Phen - + - +
LKB1 +/+ +/+ -/- -/-
G
MARK2/3
mU/mg
0.4
0.2
0
MARK2/3
Phen - + - +
LKB1 +/+ +/+ -/- -/-
H
MARK 4
mU/mg
1
0.5
0
MARK4
Phen - + - +
LKB1 +/+ +/+ -/- -/-

Figure 28

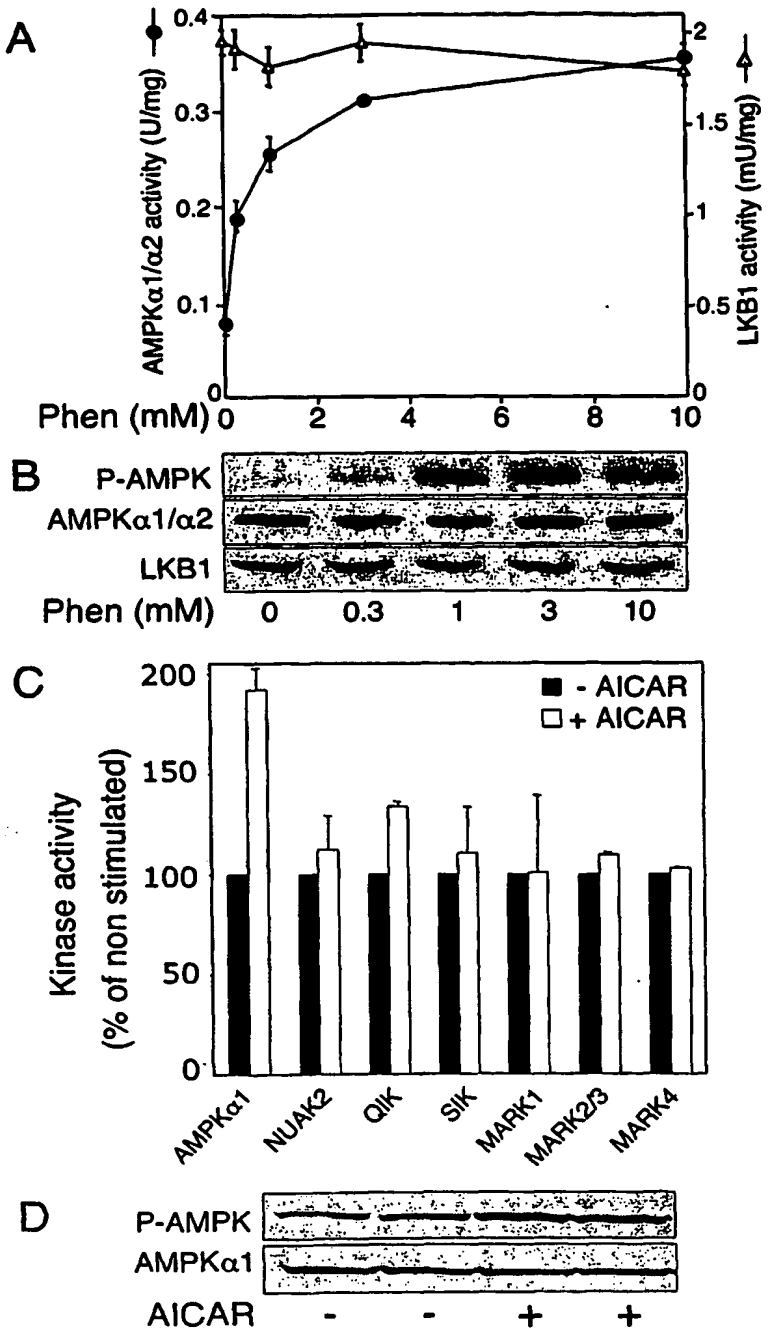

A
AMPKα1/α2 activity (U/mg)
LKB1 activity (mU/mg)
0.4
0.3
0.2
0.1
0
2
1.5
1
0.5
0
Phen (mM) 0 2 4 6 8 10
B
P-AMPK
AMPKα1/α2
LKB1
Phen (mM) 0 0.3 1 3 10
C
- AICAR
+ AICAR
Kinase activity
(% of non stimulated)
200
150
100
50
0
AMPKα1
NUAK2
QIK
SIK
MARK1
MARK2/3
MARK4
D
P-AMPK
AMPKα1
AICAR - - + +

Figure 29

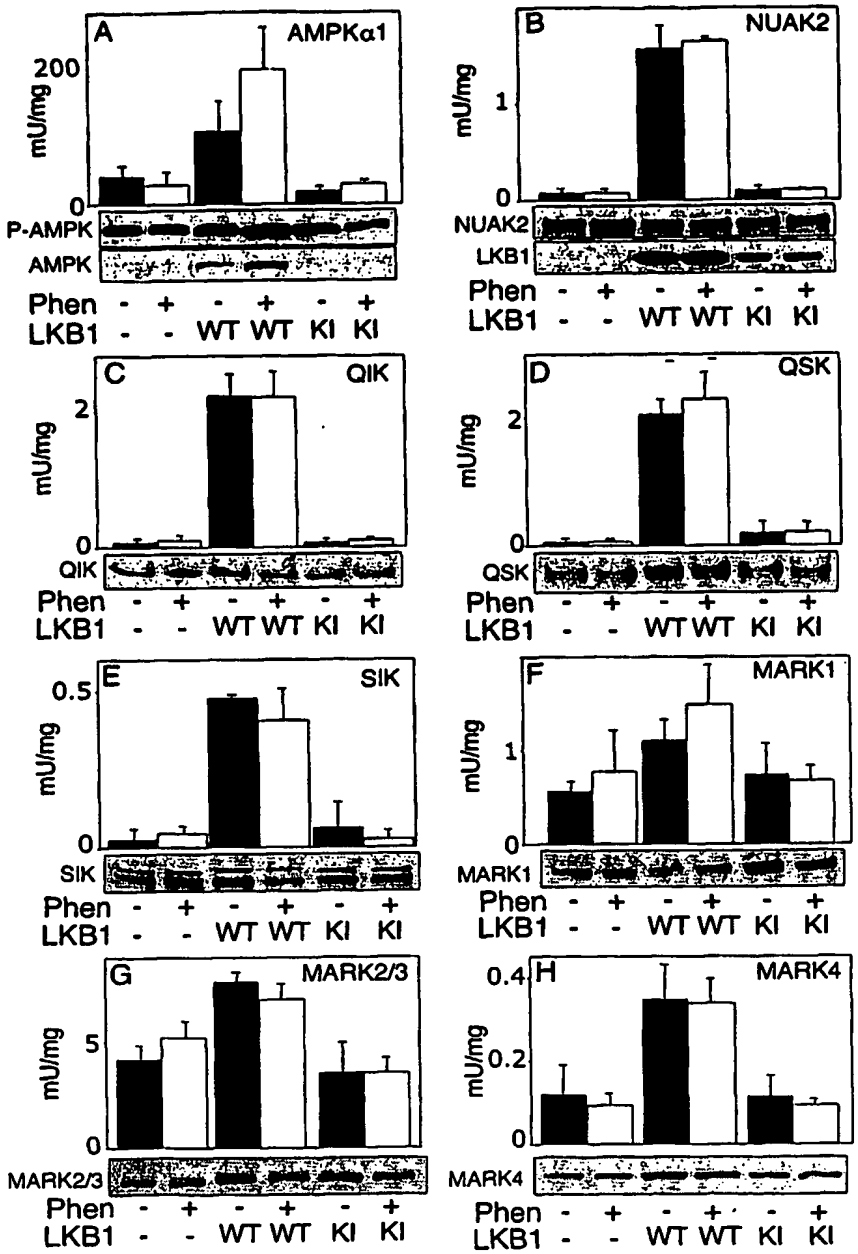
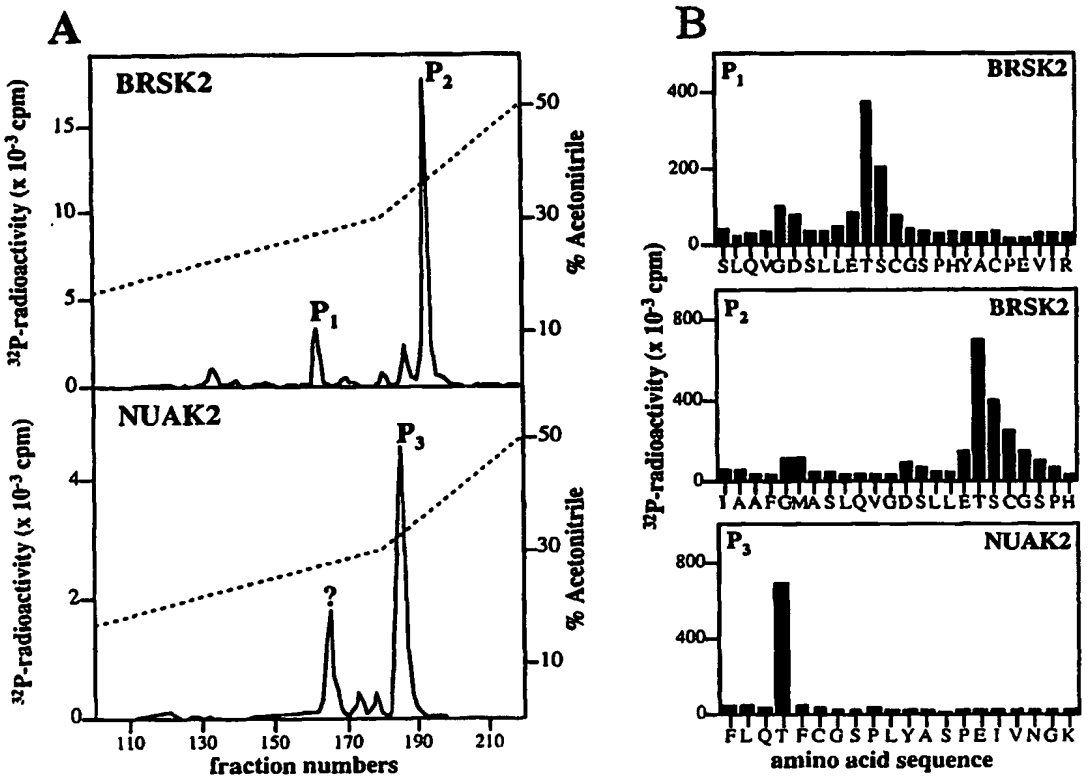

A
AMPKα1
200
mU/mg
0
P-AMPK
AMPK
Phen - + - + - +
LKB1 - - WT WT KI KI
B
NUAK2
1
mU/mg
0
NUAK2
LKB1
Phen - + - + - +
LKB1 - - WT WT KI KI
C
QIK
2
mU/mg
0
QIK
Phen - + - + - +
LKB1 - - WT WT KI KI
D
QSK
2
mU/mg
0
QSK
Phen - + - + - +
LKB1 - - WT WT KI KI
E
SIK
0.5
mU/mg
0
SIK
Phen - + - + - +
LKB1 - - WT WT KI KI
F
MARK1
1
mU/mg
0
MARK1
Phen - + - + - +
LKB1 - - WT WT KI KI
G
MARK2/3
5
mU/mg
0
MARK2/3
Phen - + - + - +
LKB1 - - WT WT KI KI
H
MARK4
0.4
0.2
mU/mg
0
MARK4
Phen - + - + - +
LKB1 - - WT WT KI KI

Figure 30



C

Kinase	Posphopeptide	Mass observed	Theoretical mass
BRSK2 P_1	IAAFGmASLQVGDSLLET(p)SCGSPHYACPEVIR	3268.7870	3628.6680
BRSK2 P_2	SLQVGDSLLET(p)SCGSPHYACPEVIR	2951.4530	2951.3472
NUAK2 P_3	FLQT(p)FCGSPLYASPEIVNGK	2356.1088	2356.1333
MARK4	LDT(p)FCGSPPYAAPELFQGK	2225.9983	2226.1497
MELK	GNKDYHLQT(p)CCGSLAYAAPELIQCK	2970.4421	2970.3648

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